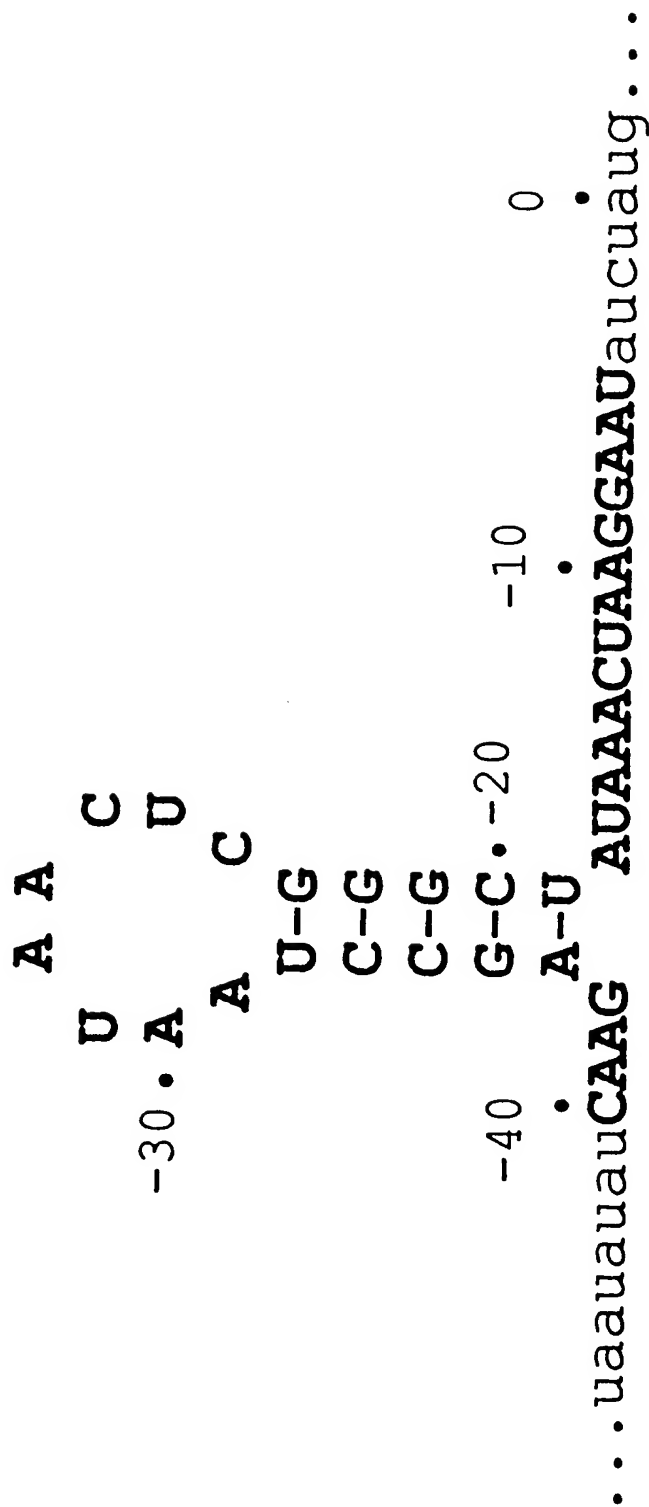


Fig. 1



SEQ. I.D. NO. 345

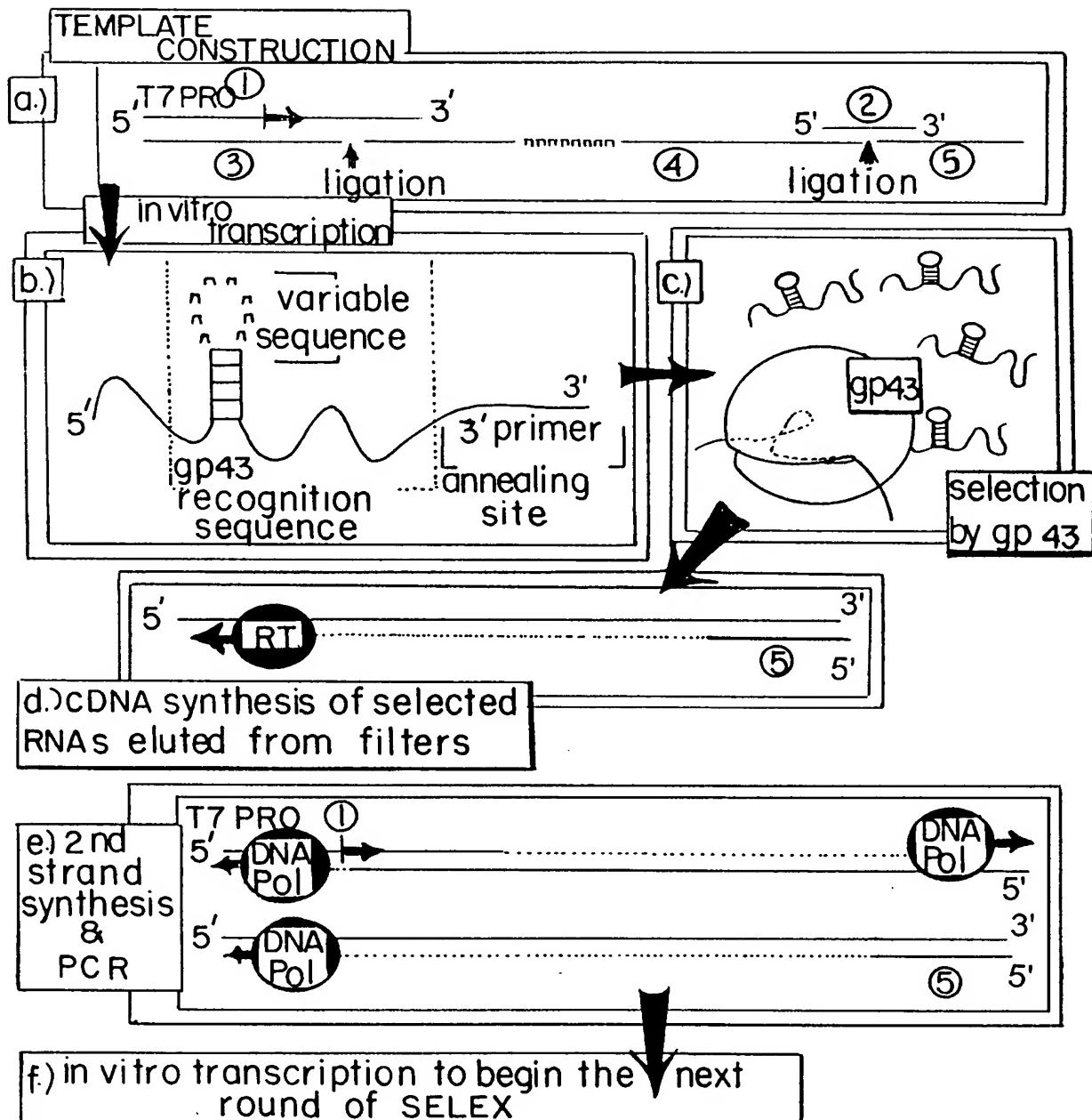


FIG.2

FIG. 3

SELECTION CYCLE:

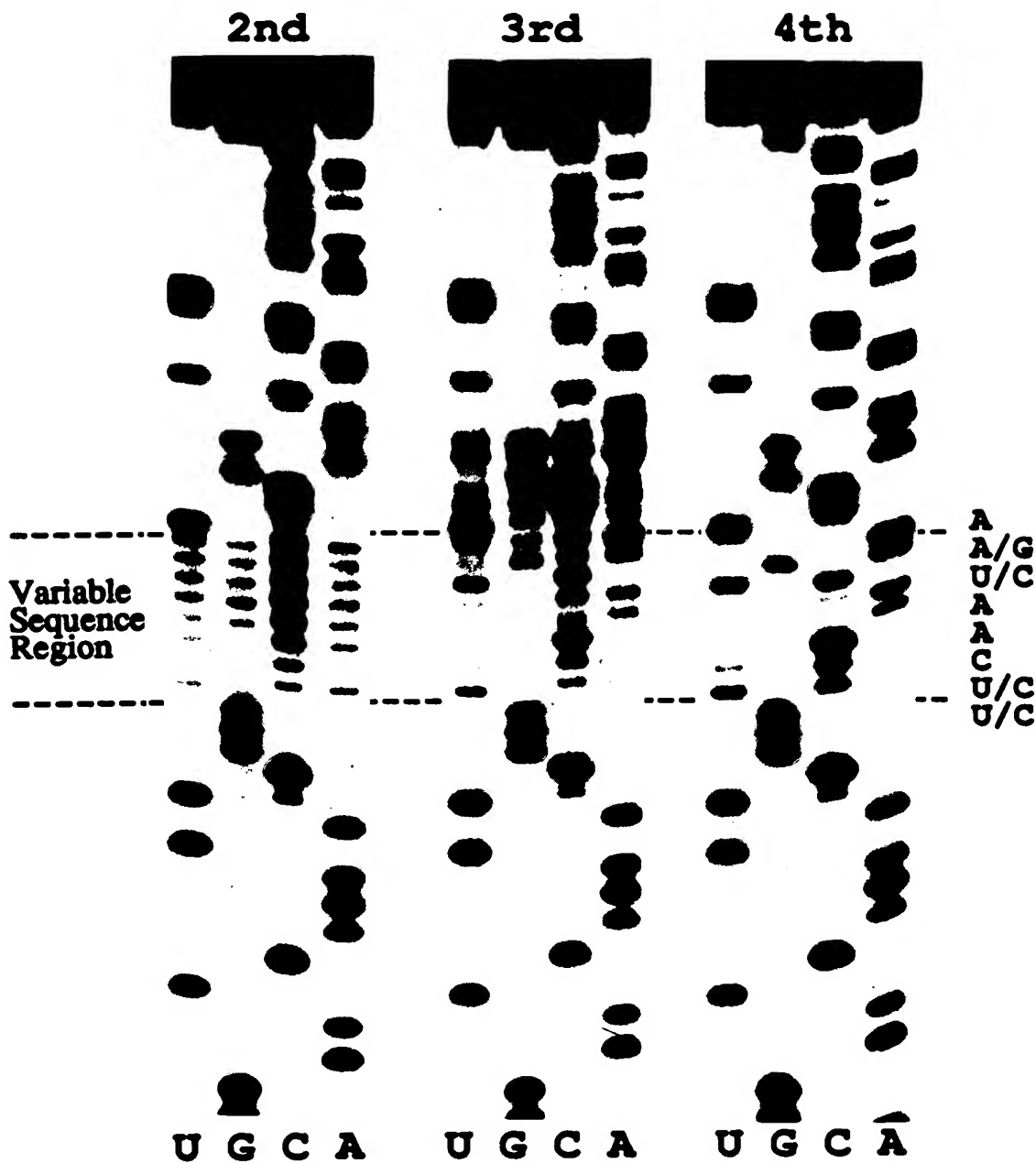


FIG. 4

EXPERIMENT:

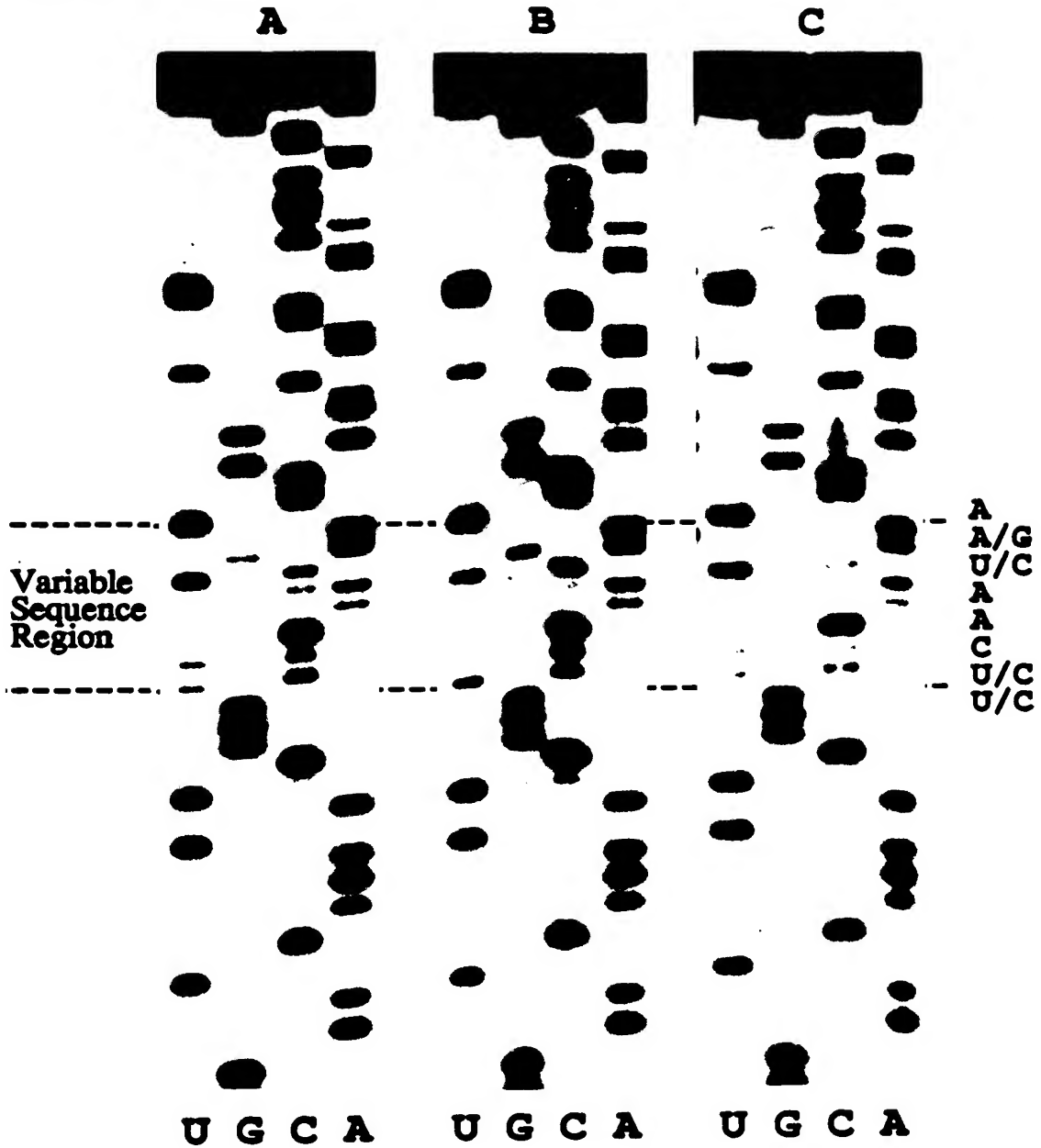


FIG. 5

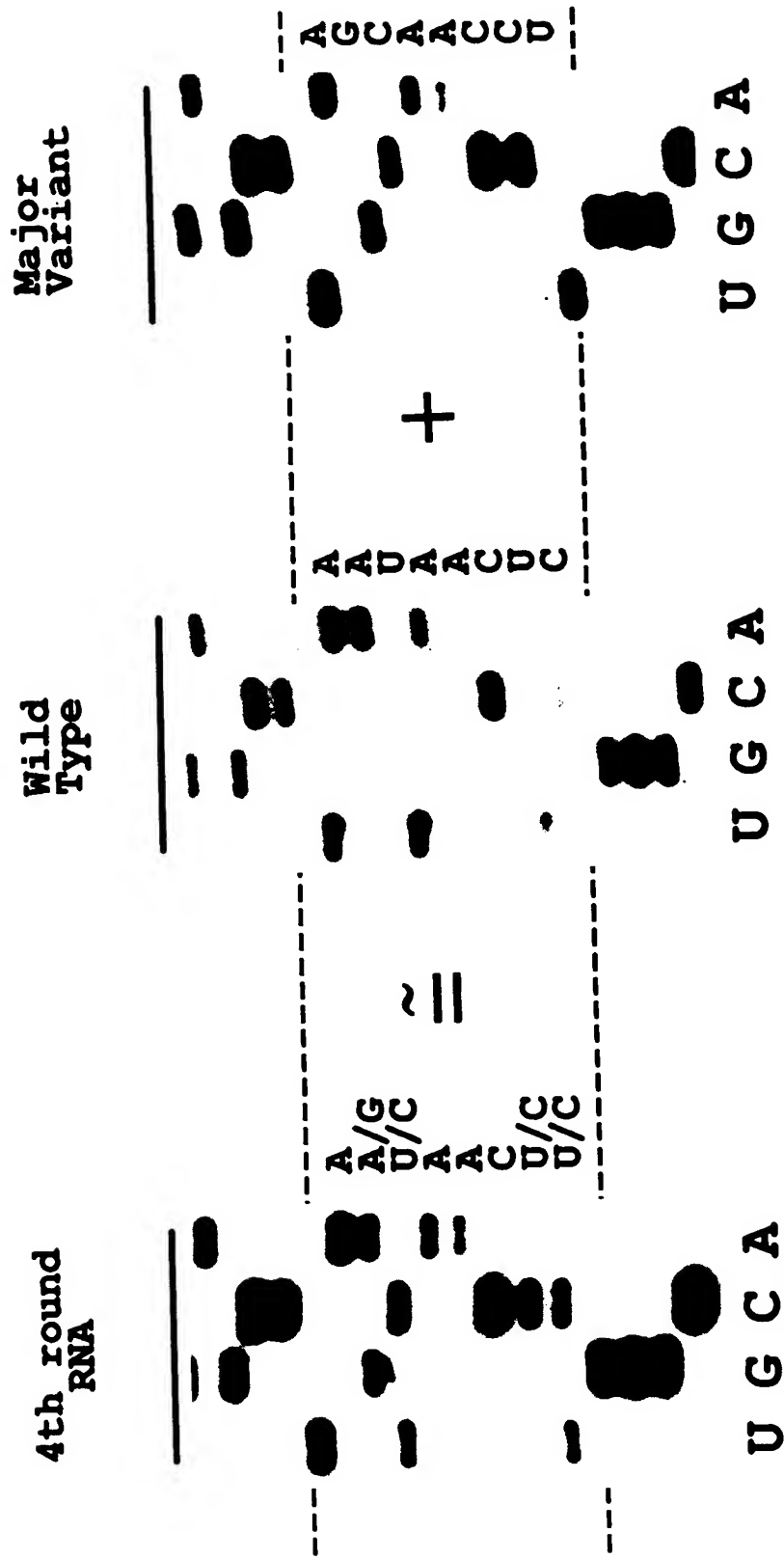
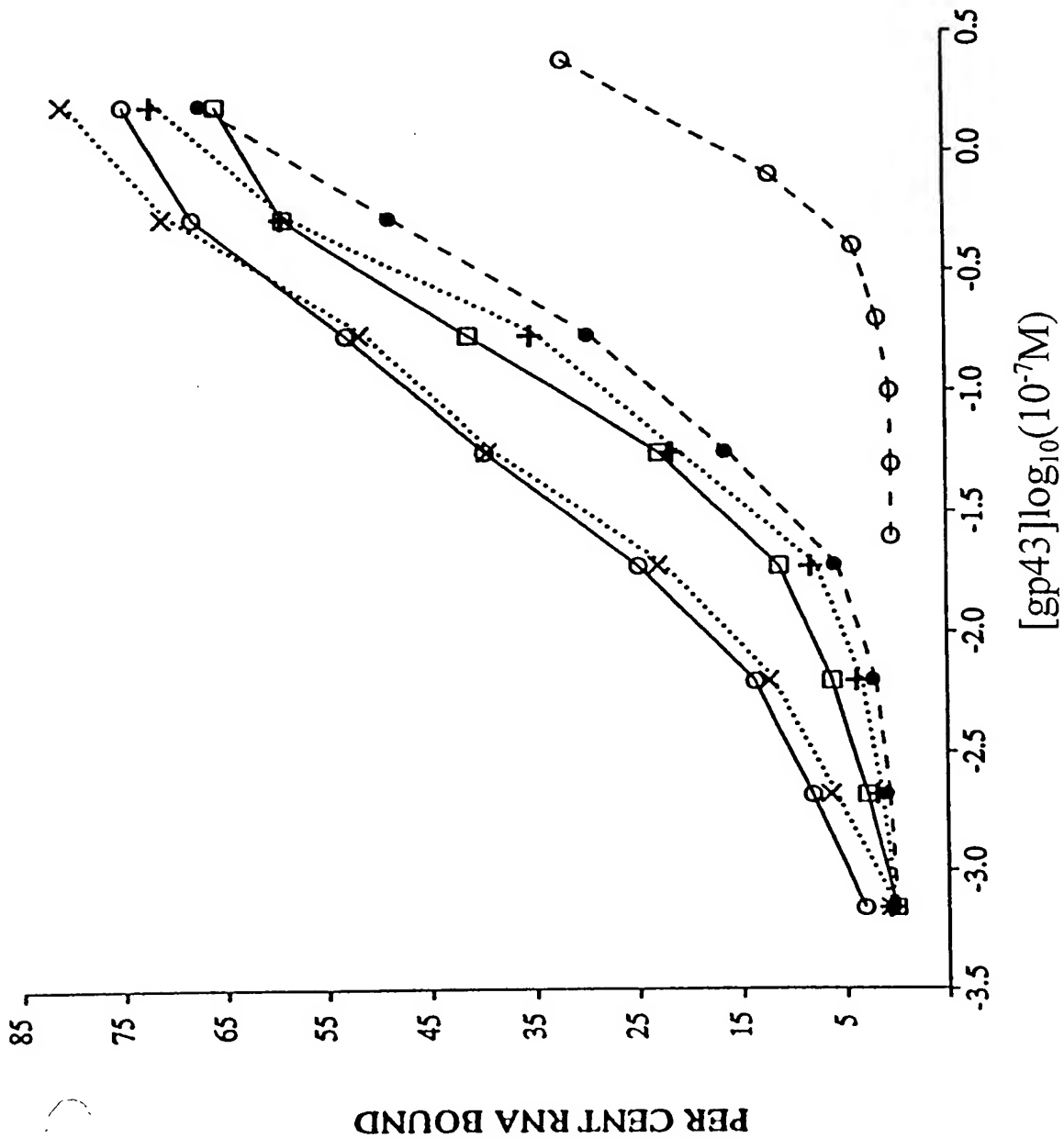


FIG. 6



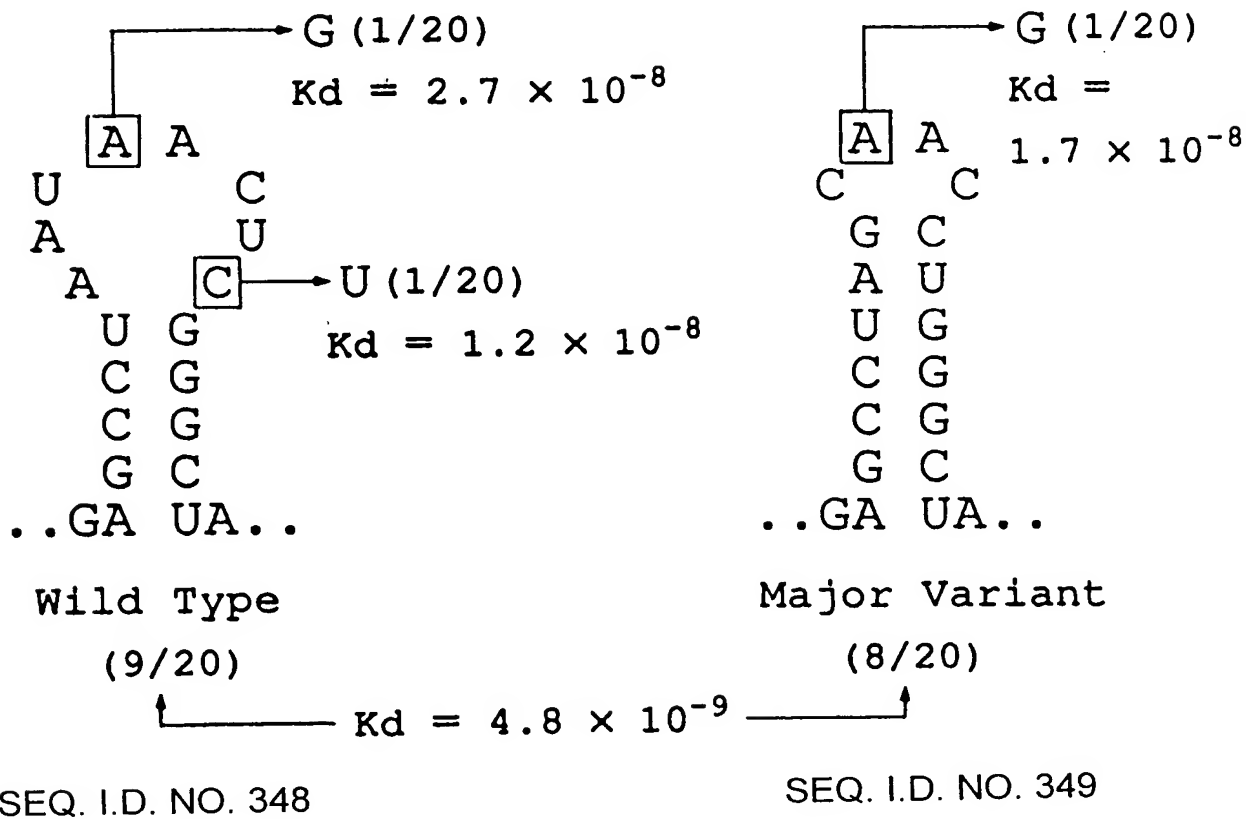
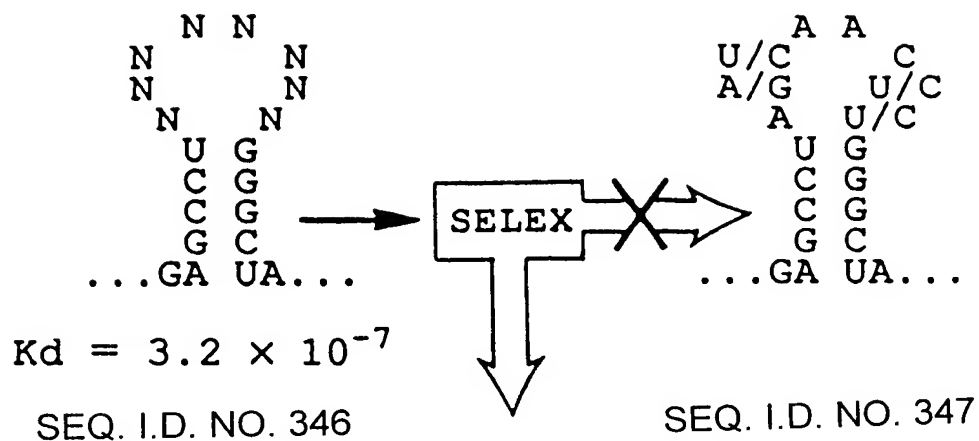


FIG. 7

VARIABLE TEMPLATE SYNTHESIS USING TERMINAL TRANSFERASE

5' PRIMER
 (OR PRIMARY LIGAND SEQUENCE) 3' 3' PRIMER 5'

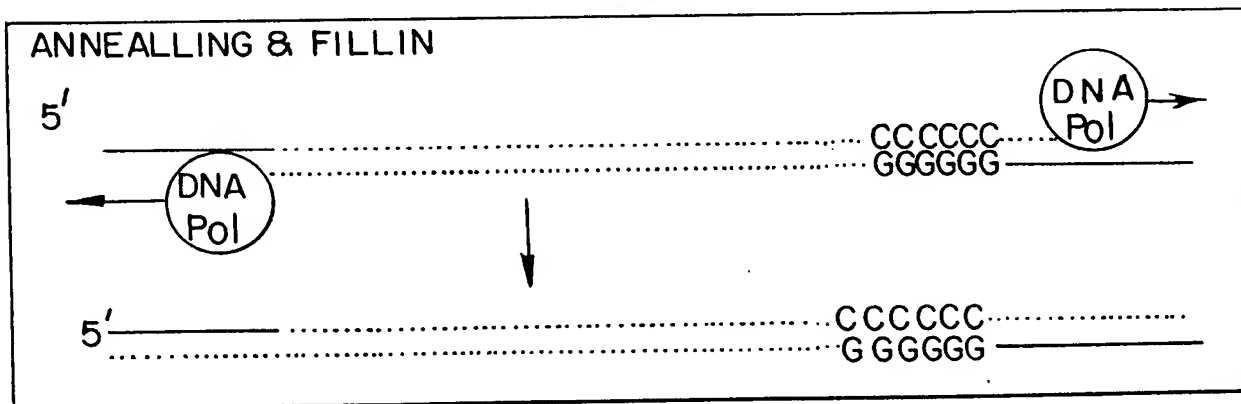
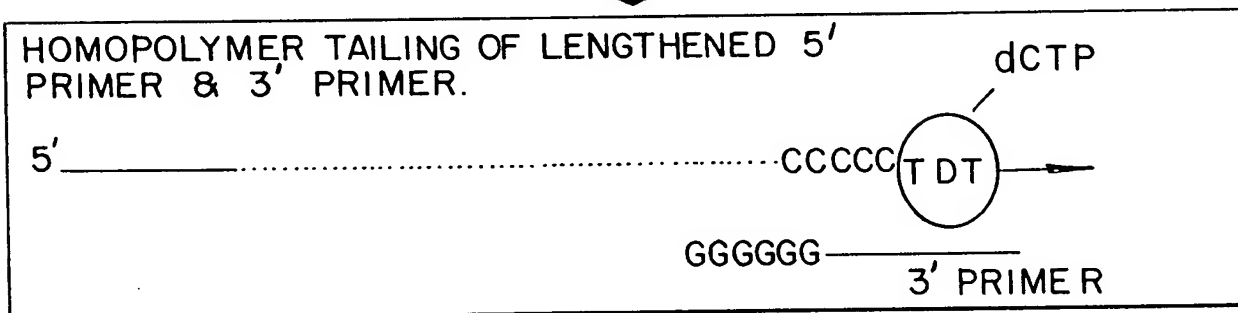
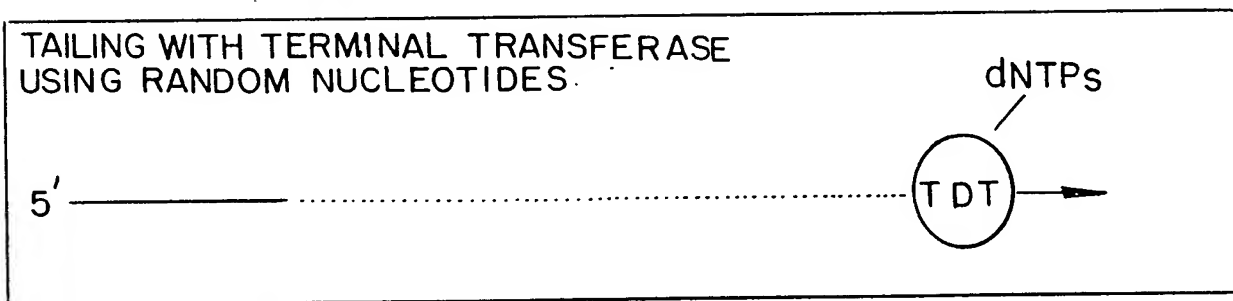


FIG. 8

"WALKING" BY EXTENDING THE PRIMARY LIGAND.

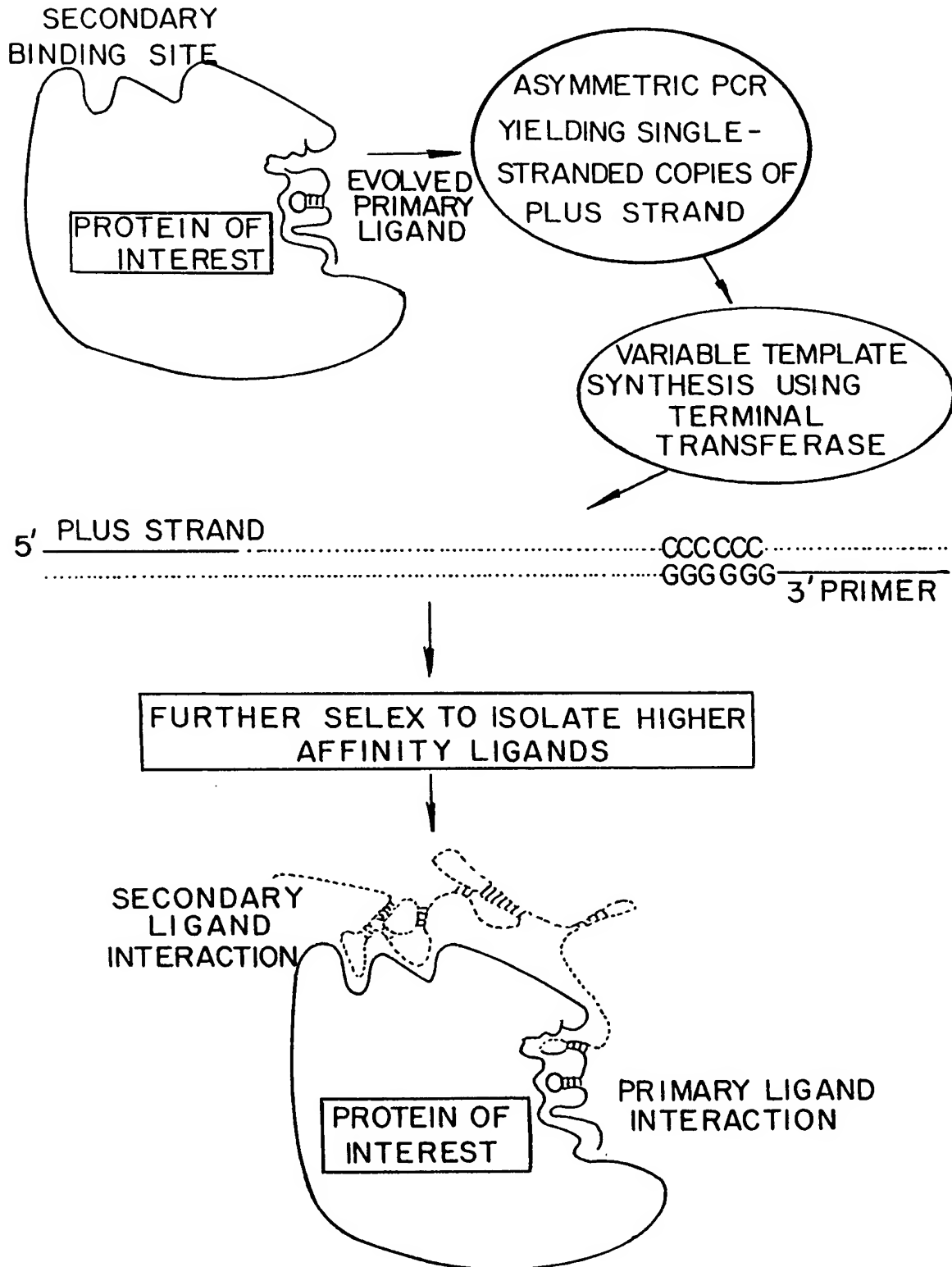
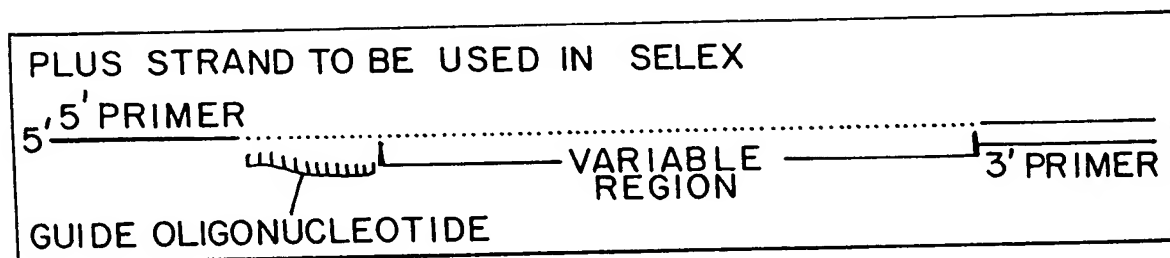
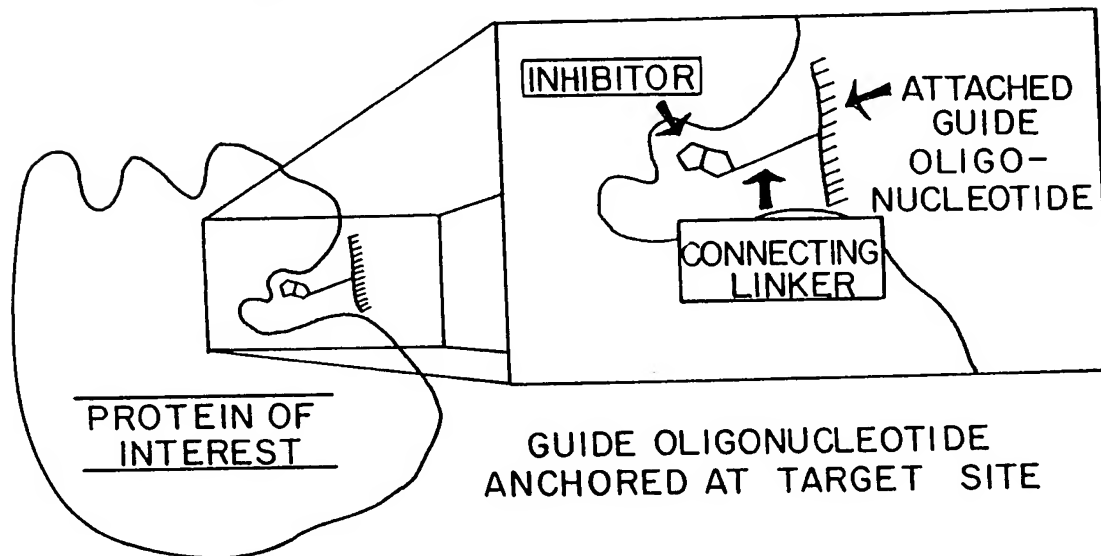


FIG.9

10037986-101801
FOR OFFICIAL USE ONLY

ANCHORING OF BRIDGING OLIGONUCLEOTIDE & SECONDARY LIGAND EVOLUTION.



SELEX LEADS TO ISOLATION OF LIGANDS THAT INTERACT WITH SECONDARY BINDING SITES

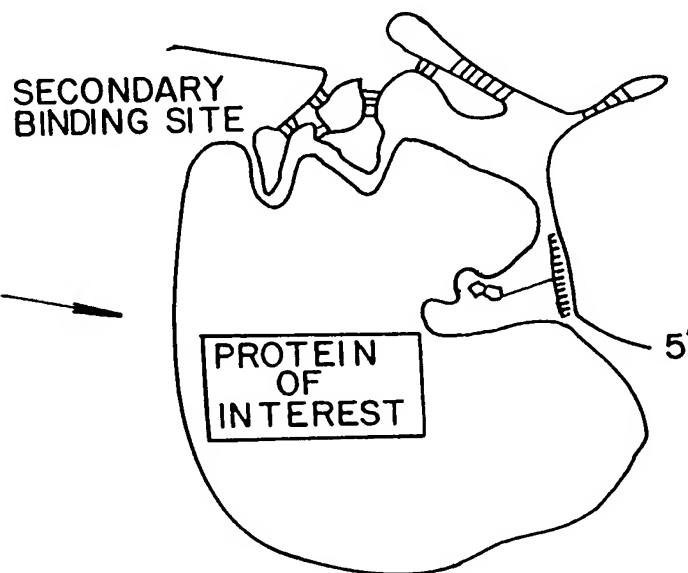


FIG.10

10037965-101001

SECONDARY LIGAND-DIRECTED PRIMARY LIGAND EVOLUTION.

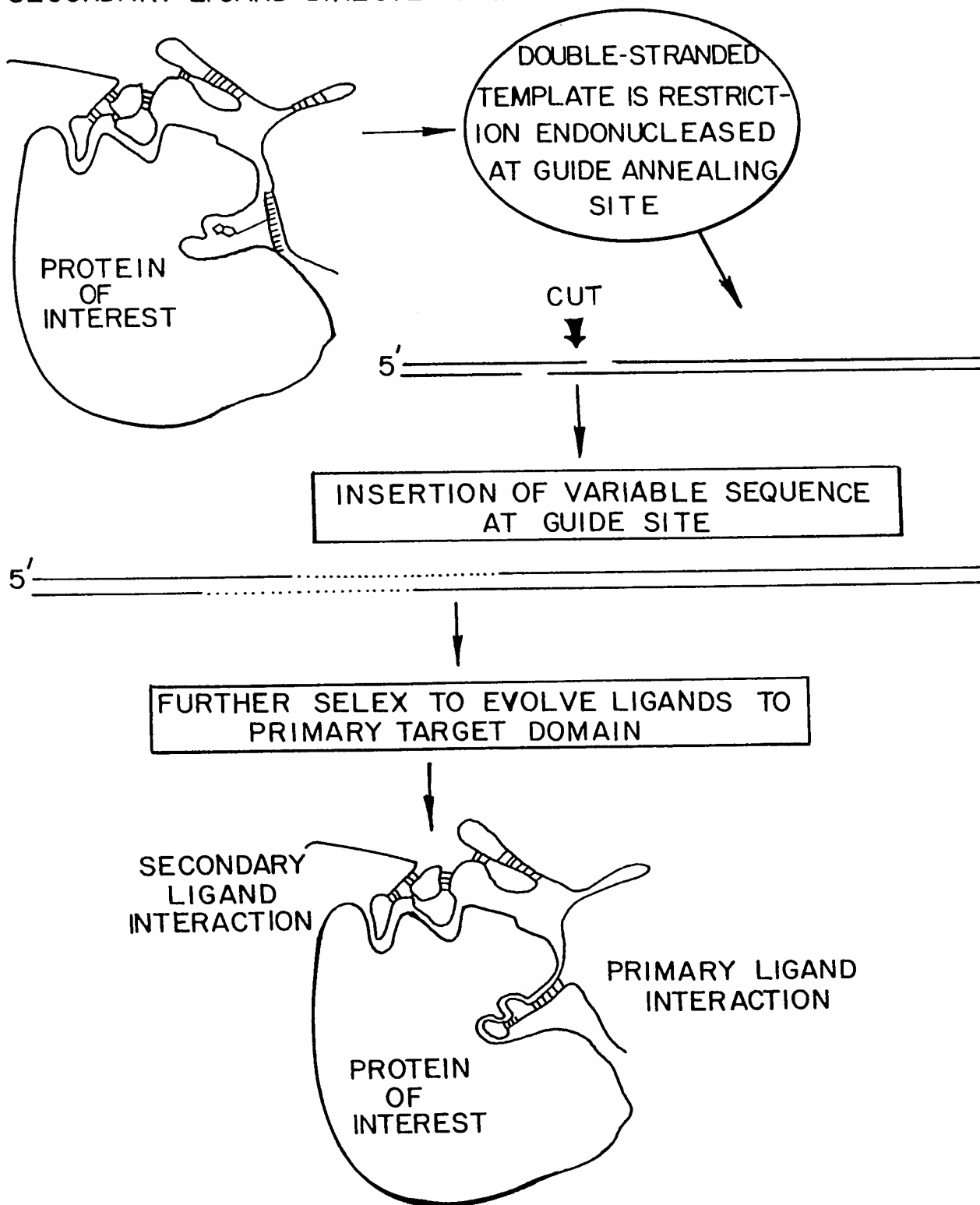
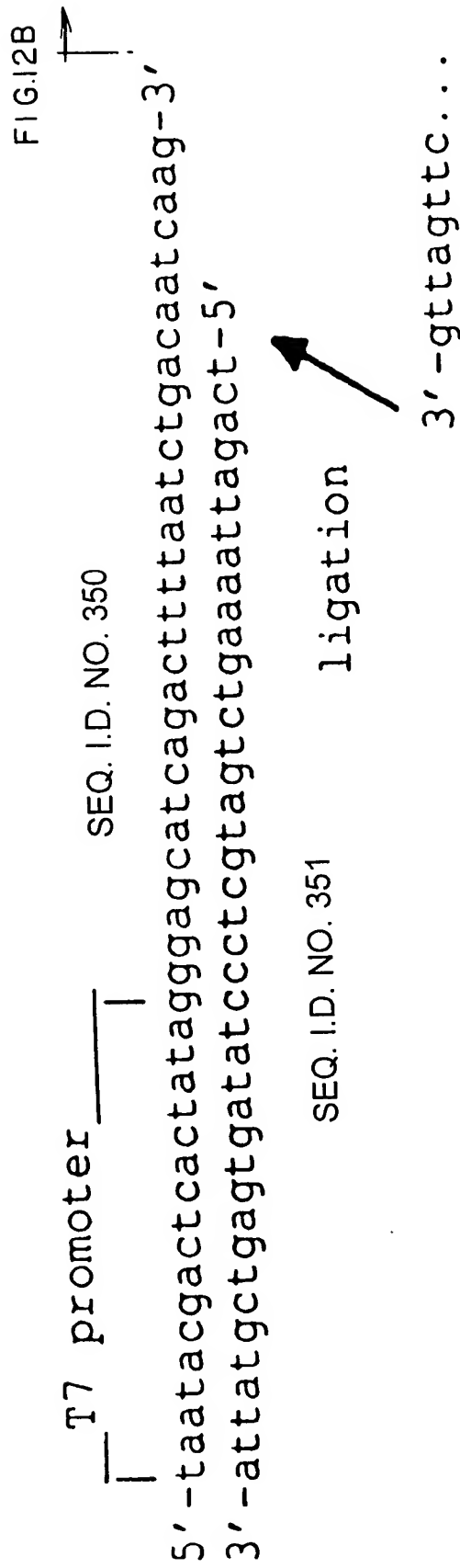


FIG.11

10037986.101801



FOOT" 986/FOOT

← 12A

5'-atctatgaaagaattttatatctc-3'

3'-cttaaaatatagagataactttgcctaggcc-5'

SEQ. I.D. NO. 352

ligation



32n..tagatacttt-5'

SEQ. I.D. NO. 353

uuauaucucuauugaaacggaucgg-3'

← 12A

SEQ. I.D. NO. 354

FIG. 12B

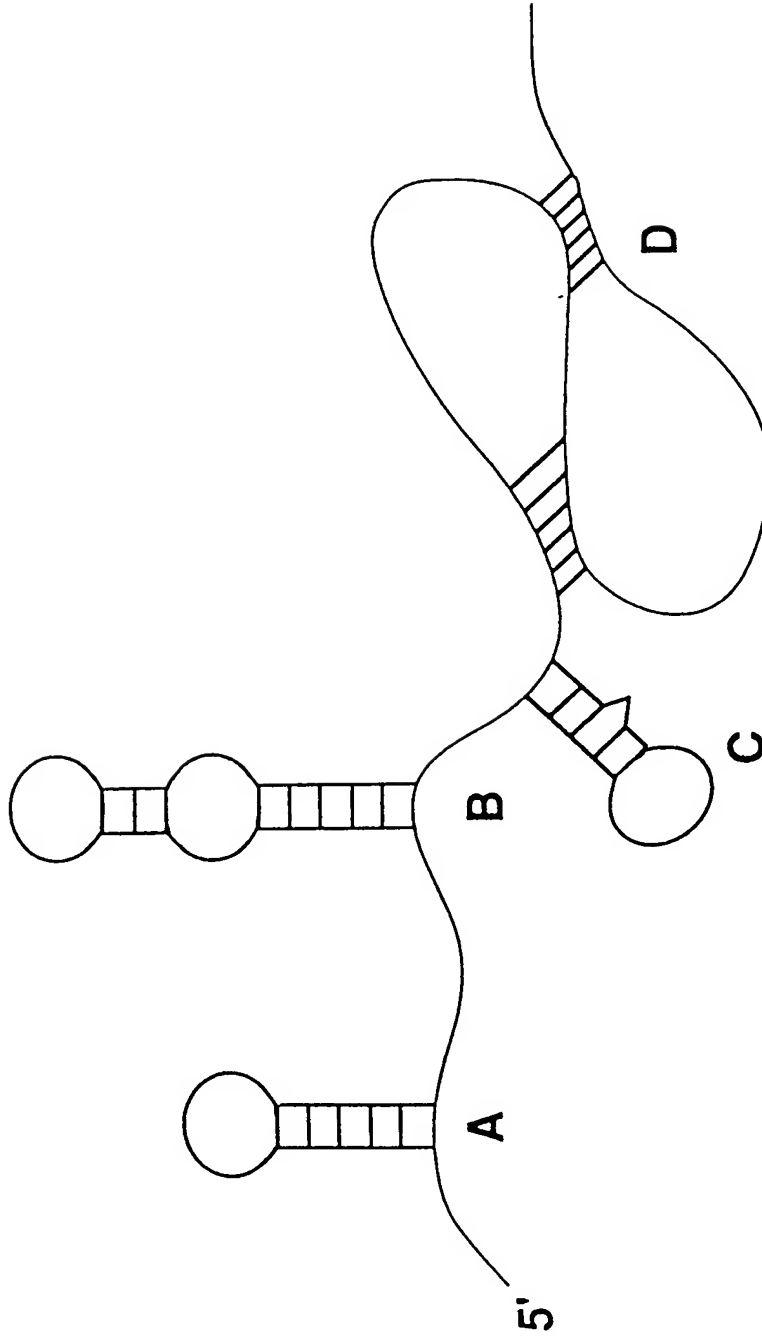
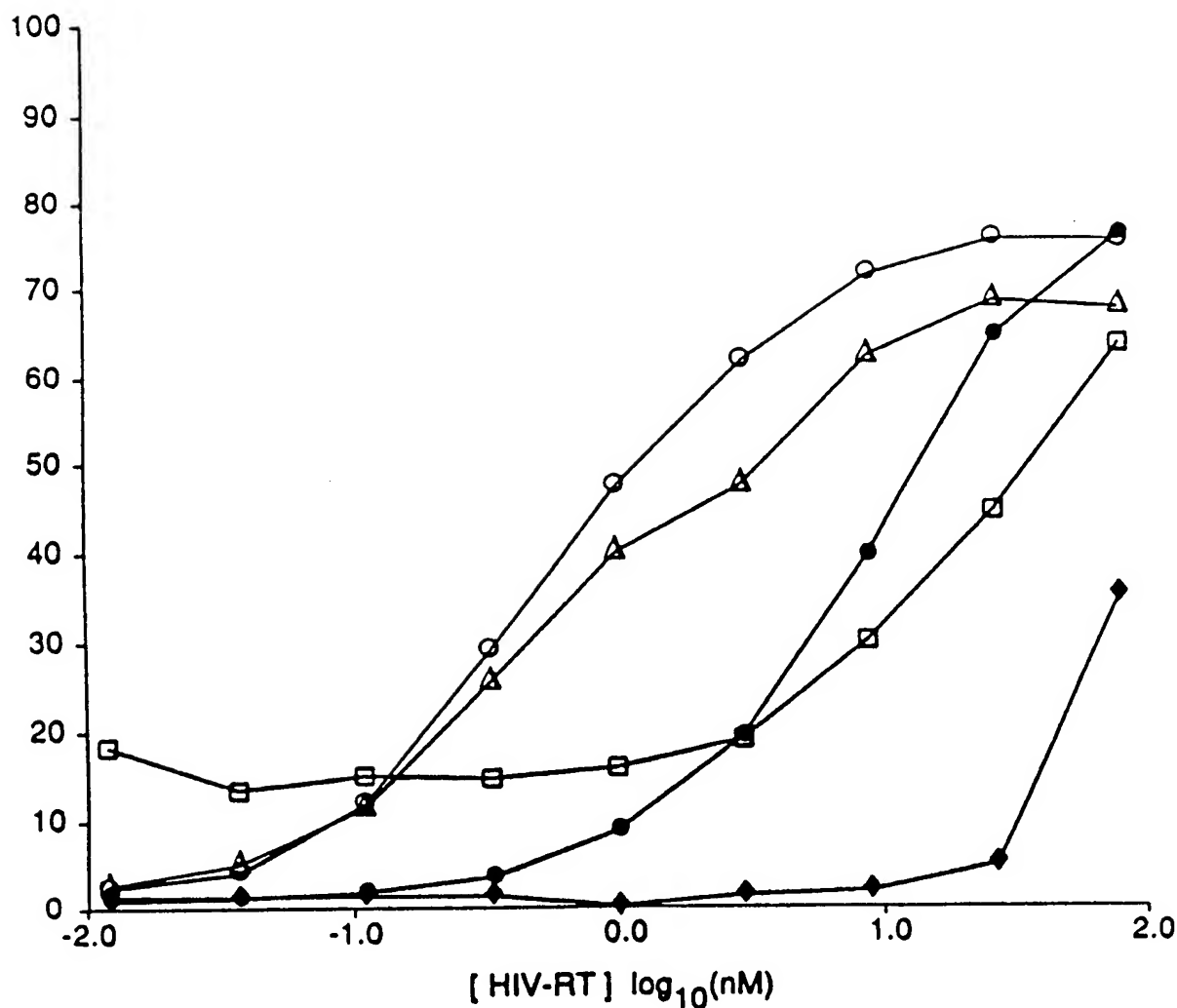


FIG.13

FIG.14



Δ 1.1 ucaagAAUUCCGUUUUCAGUCGGGAAAAACUGAACA ducu (13)

○ 1.3 ucaagAAUAUCUUCCGAAGCCGAACGGGAAAACCGG'Caucu (1)

● 1.3 -----G-----A----- (1)

□ 1.4 ucaagGGCAUCUGGGAGGGUAAGGGUAAGGUUGUCGGaucu (4)

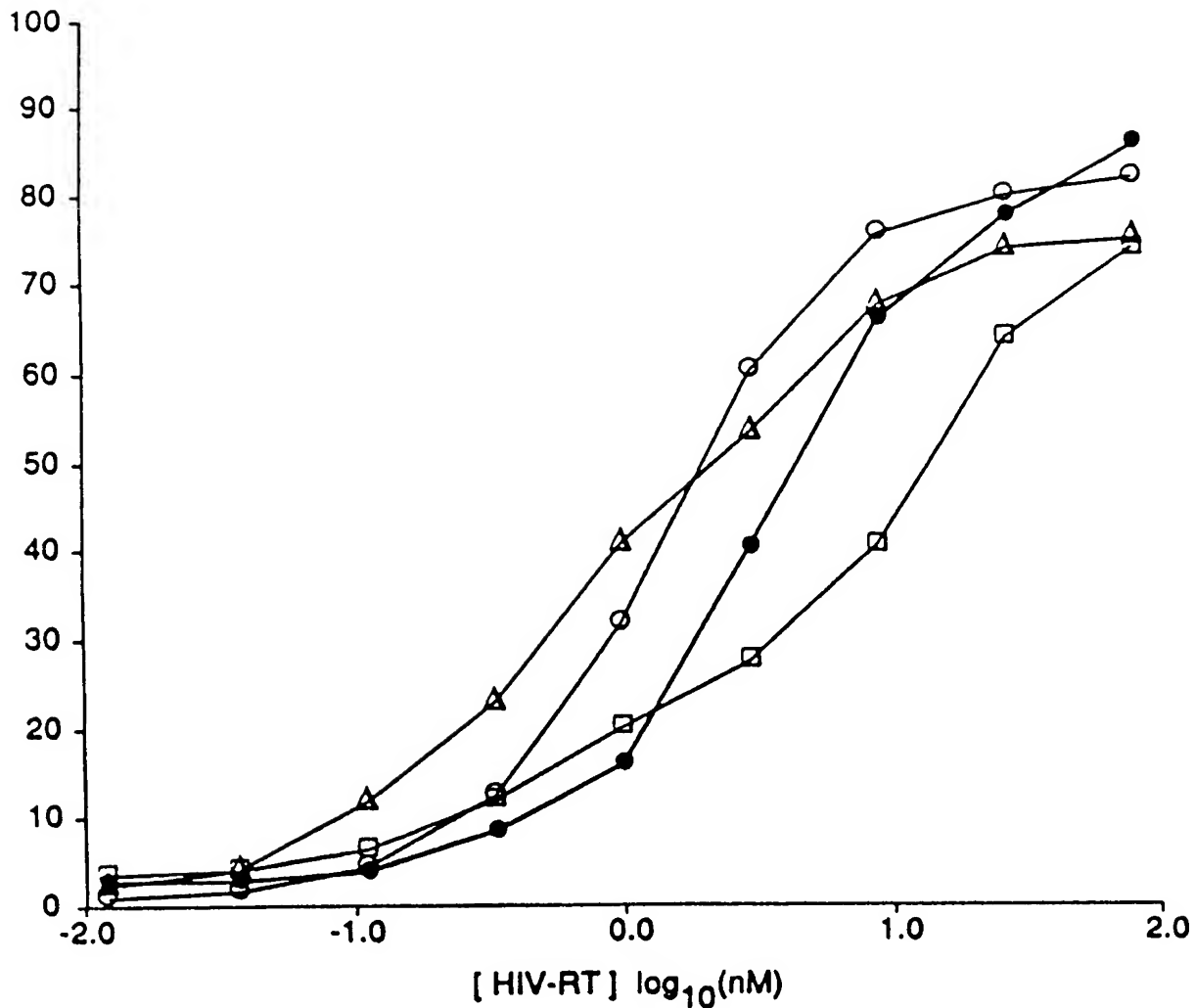
Δ 1.1 = SEQ. I.D. NO. 355

● 1.3 = SEQ. I.D. NO. 357

○ 1.3 = SEQ. I.D. NO. 356

□ 1.4 = SEQ. I.D. NO. 358

FIG.15



ISOLATE

○ 2.1a ucaag--AAUAUA-UCCGAACUCGACGGGAUAACGAGAA-Gaucu (3)

□ 2.2b ucaagUACCUAGGUGAUAAAGGGAGAACACGUGUGa-cu (13)

● 2.5b ucaagACAGUAUCCGUUCUUGAUCAUCGGGACAAAUGaucu (3)

△ 1.1 ucaagAAUUCCGUUUUCAGUCGGGAAAACUGAACAAUcu (13)

○ 2.1a = SEQ. I.D. NO. 359

● 2.5b = SEQ. I.D. NO. 361

□ 2.2b = SEQ. I.D. NO. 360

△ 1.1 = SEQ. I.D. NO. 362

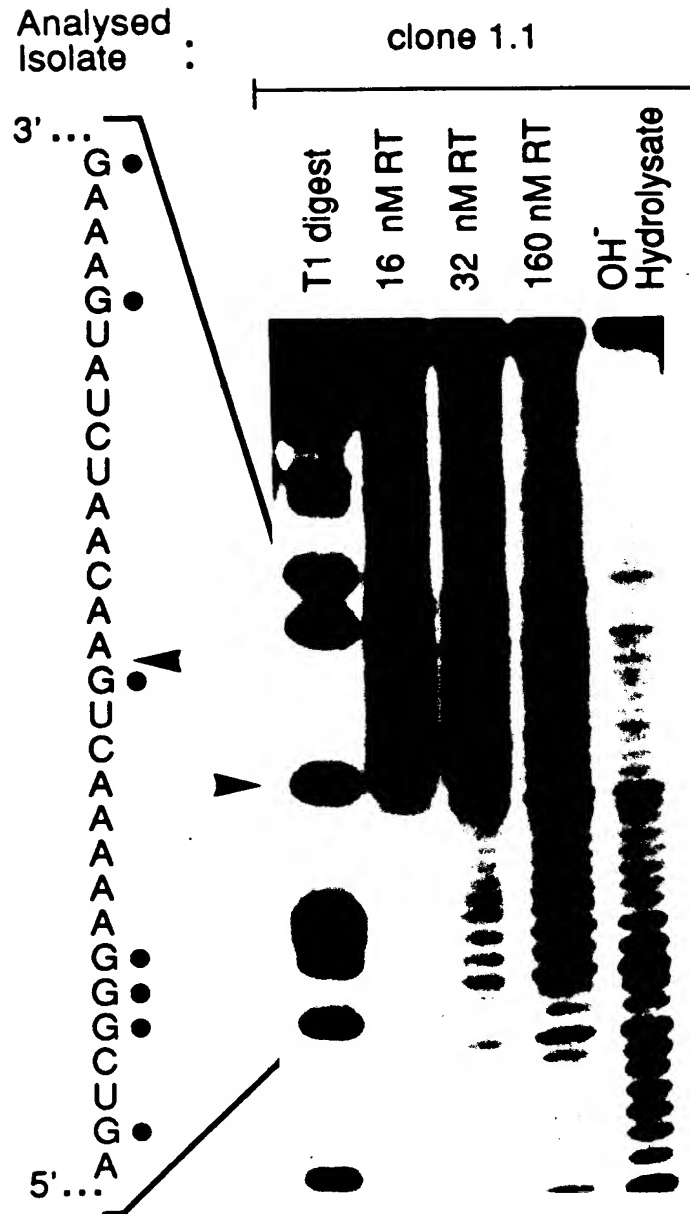


FIG. 16 A

SEQ. I.D. NO. 363

108701 985/007

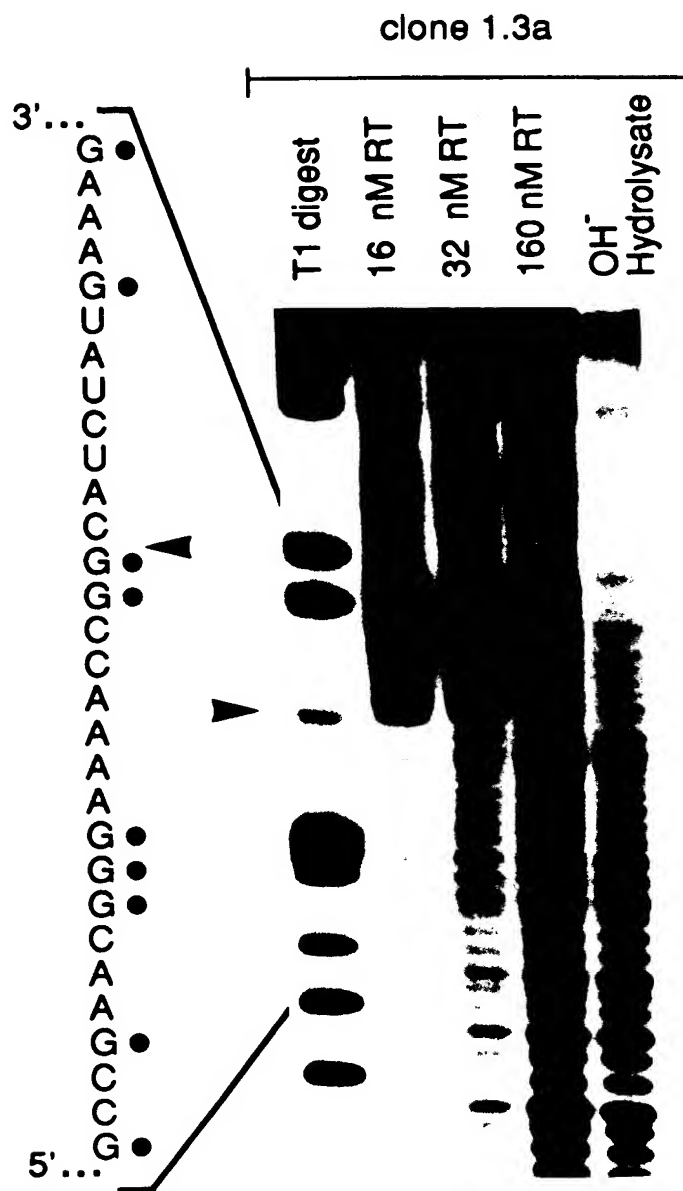
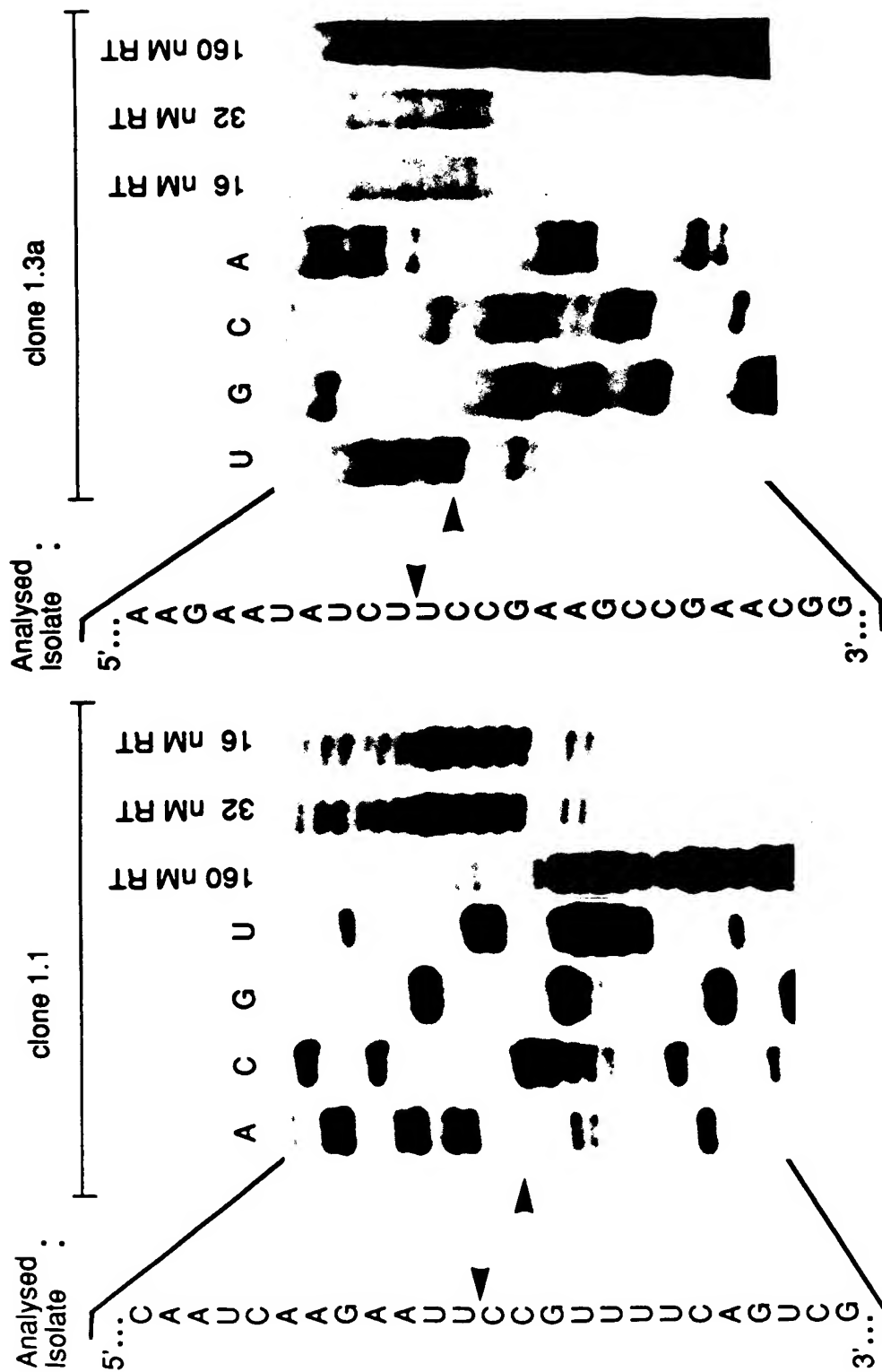


FIG.16 B

SEQ. I.D. NO. 364

10037986-101304

FIG.16 C



SEQ. I.D. NO. 366

SEQ. I.D. NO. 365

FOR FOOT 9864E00T

FIG. 17B

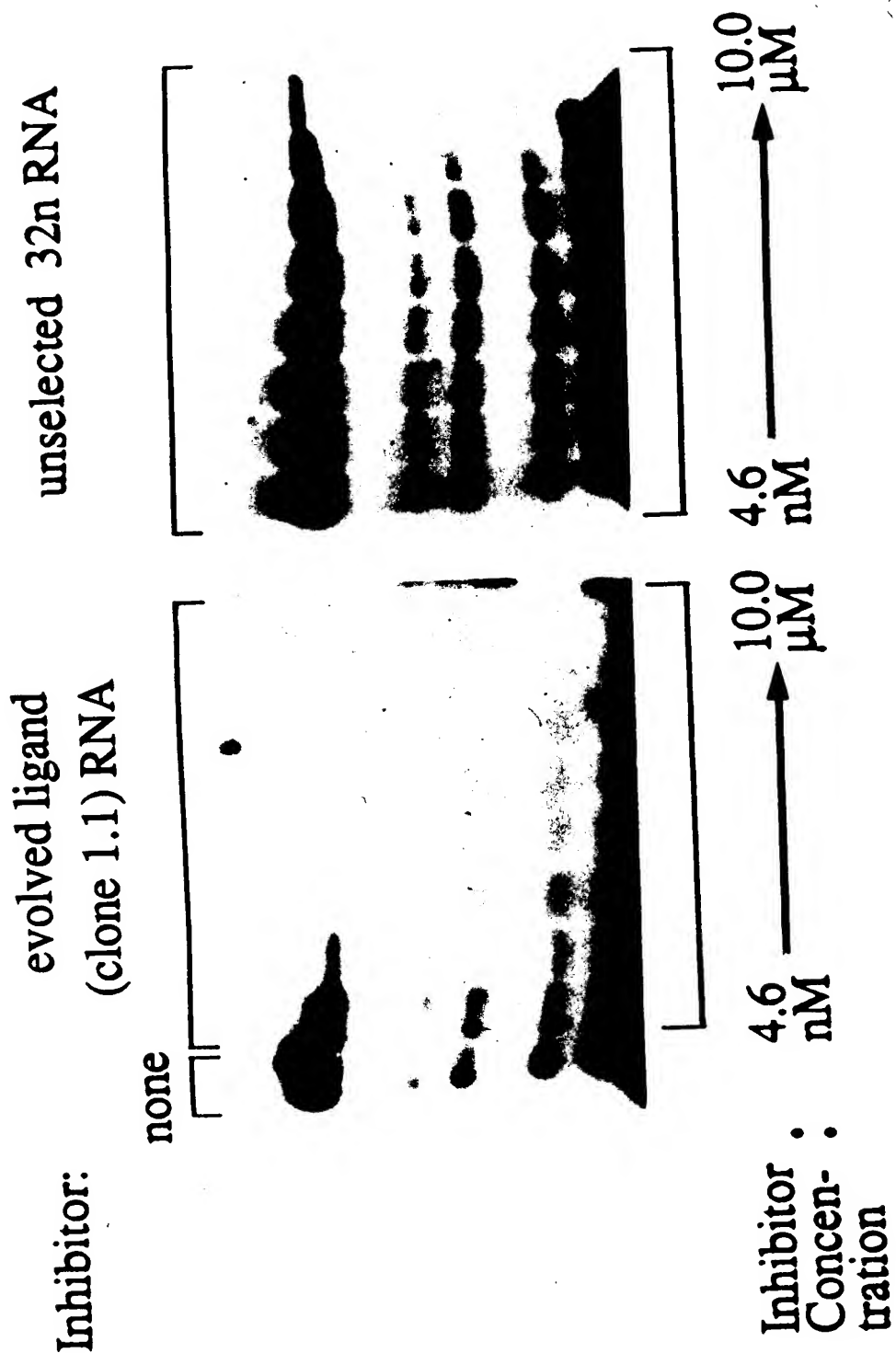


FIG.18

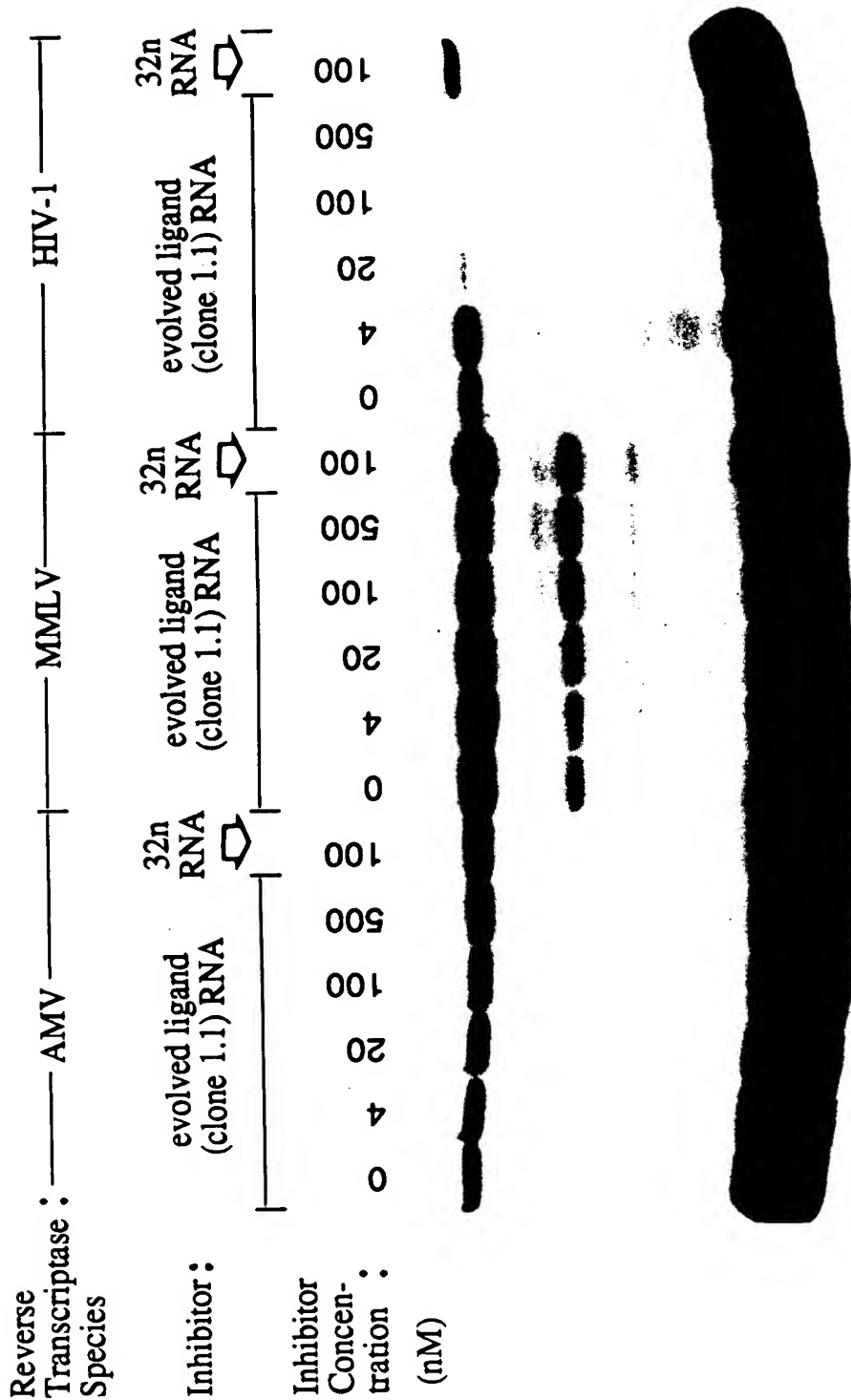
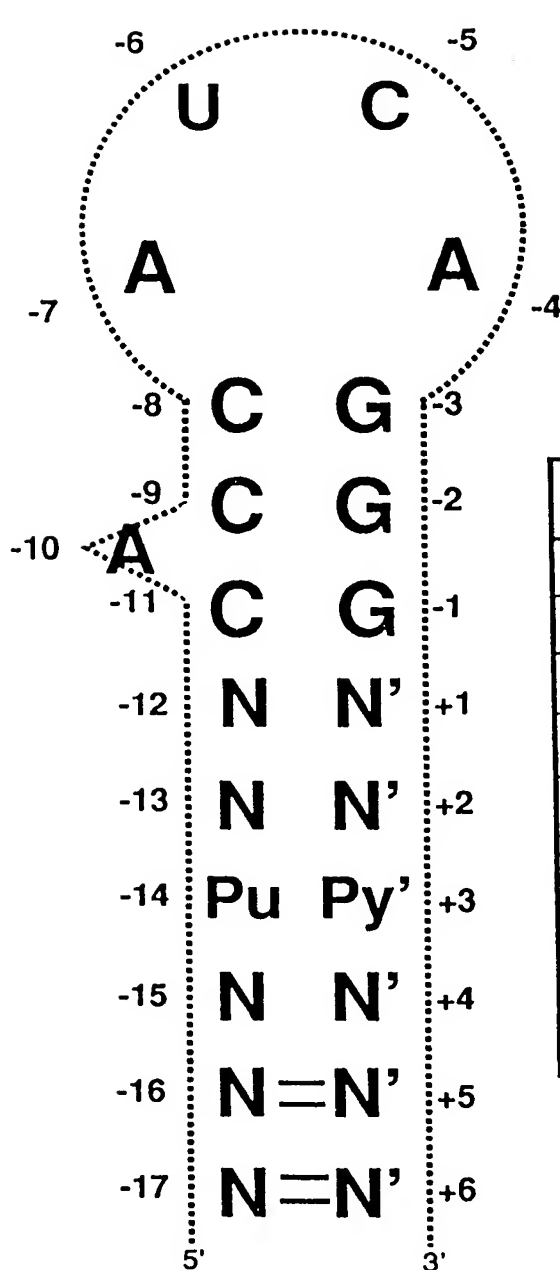


FIG.19B



	A	C	G	U
-4	36	0	0	0
-5	0	36	0	0
-6	4	3	1	28
-7	36	0	0	0
-10	36	0	0	0

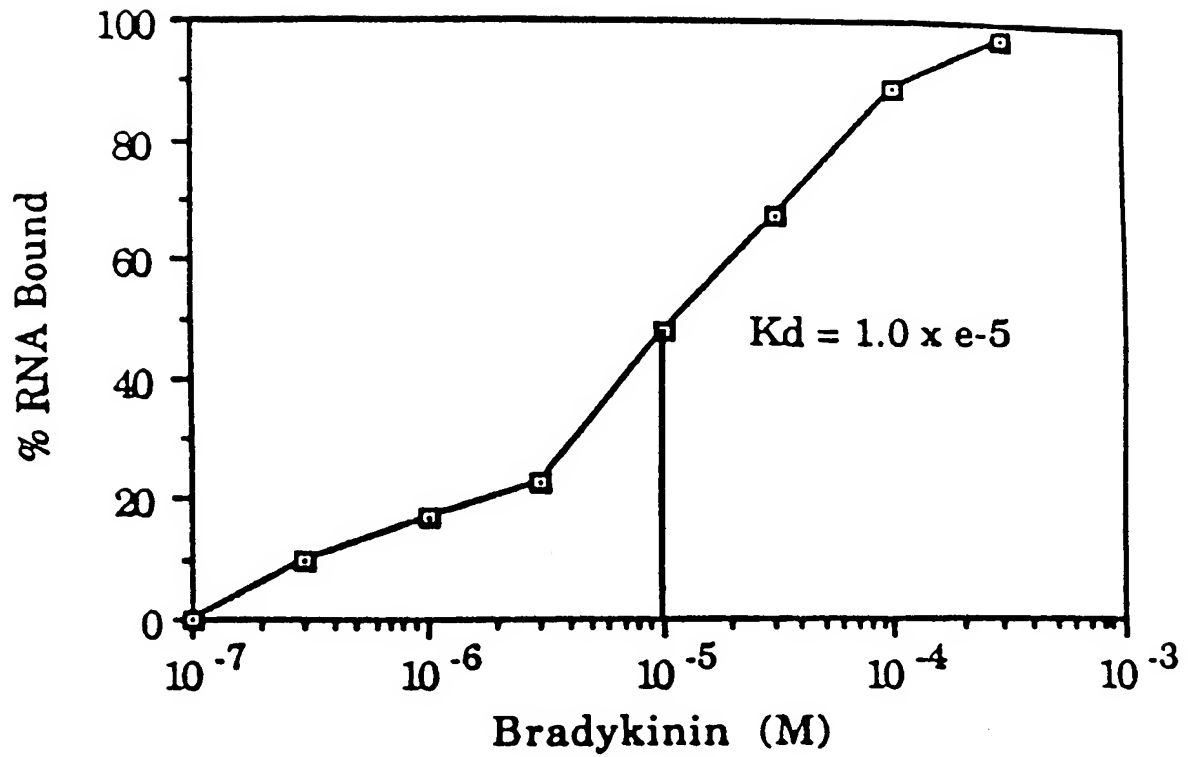
	AU	CG	UA	GC	UG	GU	Bulge	END
-8/-3	0	24	0	12	0	0	0	0
-9/-2	0	25	0	10	1	0	36	0
-11/-1	0	24	2	10	0	0	0	1
-12/+1	8	1	8	10	7	1	3	3
-13/+2	6	5	8	9	3	1	3	4
-14/+3	9	0	4	10	2	3	6	8
-15/+4	4	0	9	6	0	1	0	2
-16/+5	10	1	2	1	1	3	1	1
-17/+6	0	4	6	1	4	2		

FIG.19C

FIG.19A

SEQ. I.D. NO. 367

FIG.20



FOOT" 9862E00T

FIG.21A

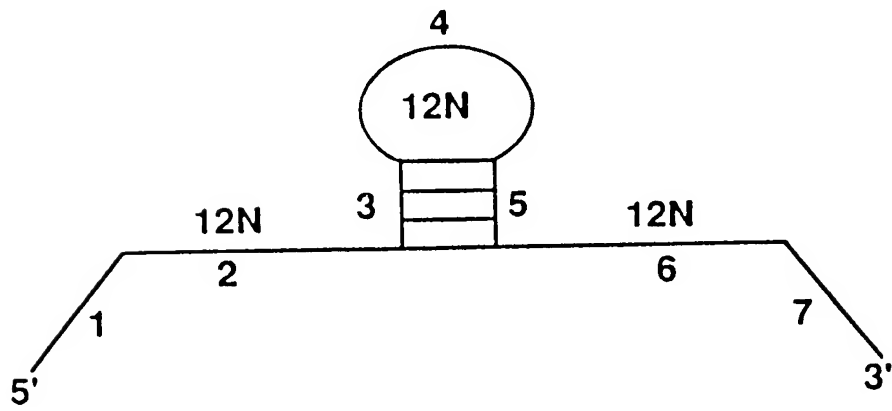
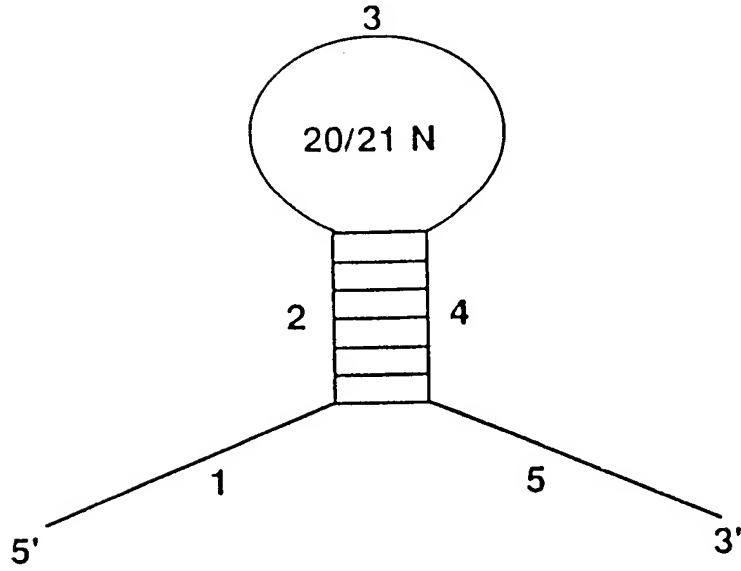


FIG.21B

10037986-101301

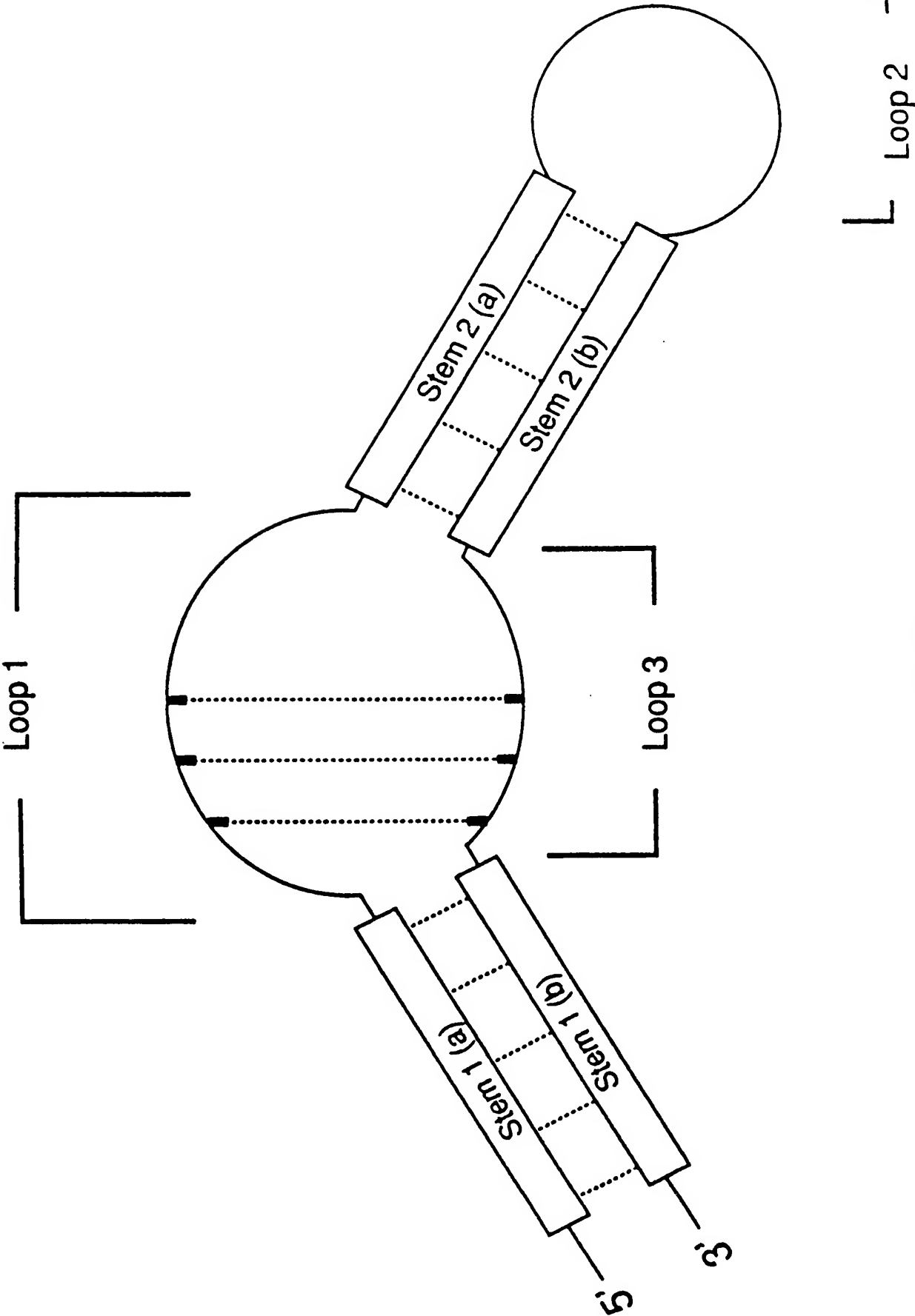


FIG.22

10037986-101801

Motif I (6a)

UUGAGAAA G
 5' ... gGGUGCA ||| CAC U (NUCLEOTIDES 2-38 OF SEQ. I.D. NO. 301)
 3' ... ucuaUGU ||| GUG U
 --CUCA-G U

Motif III (9a)

CC UUGaucua-
 A GG ||||| uga-3'
 A CC ||||| GCUU-5'
 UU --CUAGUAA

Motif II (1c)

AAGAUU UCU
 5' ... AGAUG CAGC
 3' ... ucuaC GUCC A
 -ACA-G UAG

SEQ. I.D. NO. 369

SEQ. I.D. NO. 368

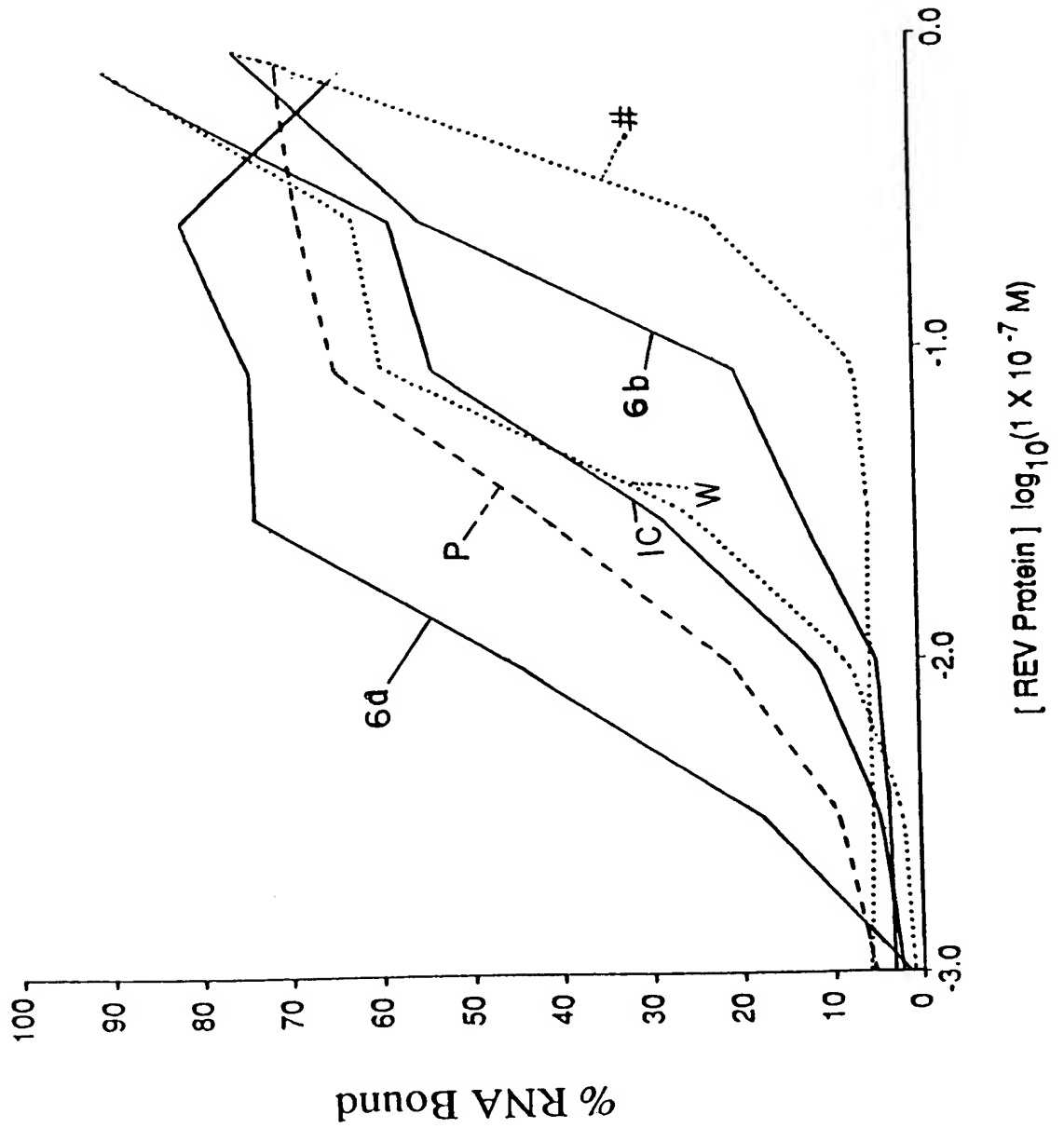
WT (Motif II-like Domain)

U ACGGUA
 A GACGCUG || CA...3'
 CUGCGAC || GU...5'
 A -GCG-G

SEQ. I.D. NO. 370

FIG. 23

FIG. 24



FOOTNOT 9862E00T

FIG. 25

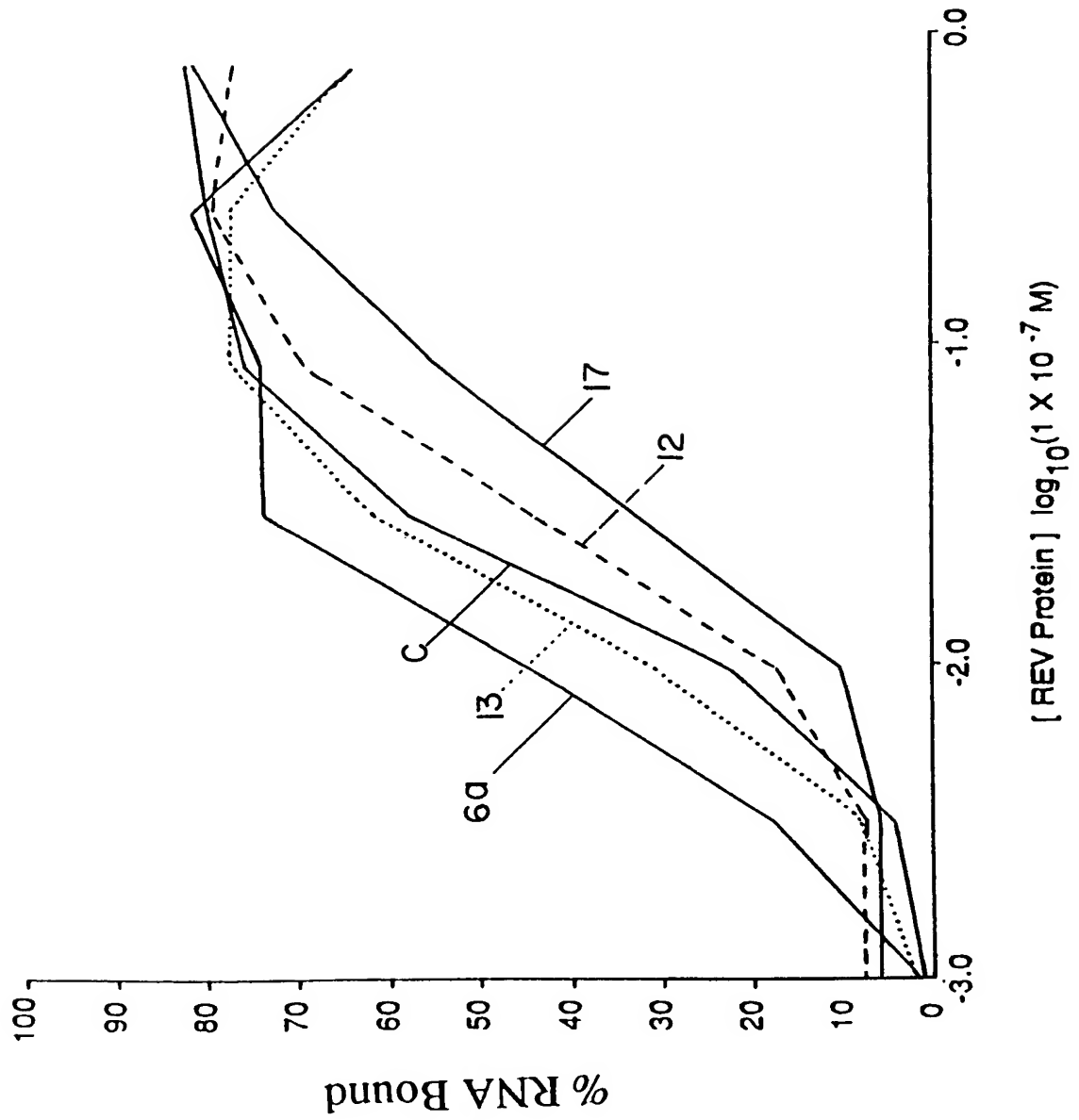
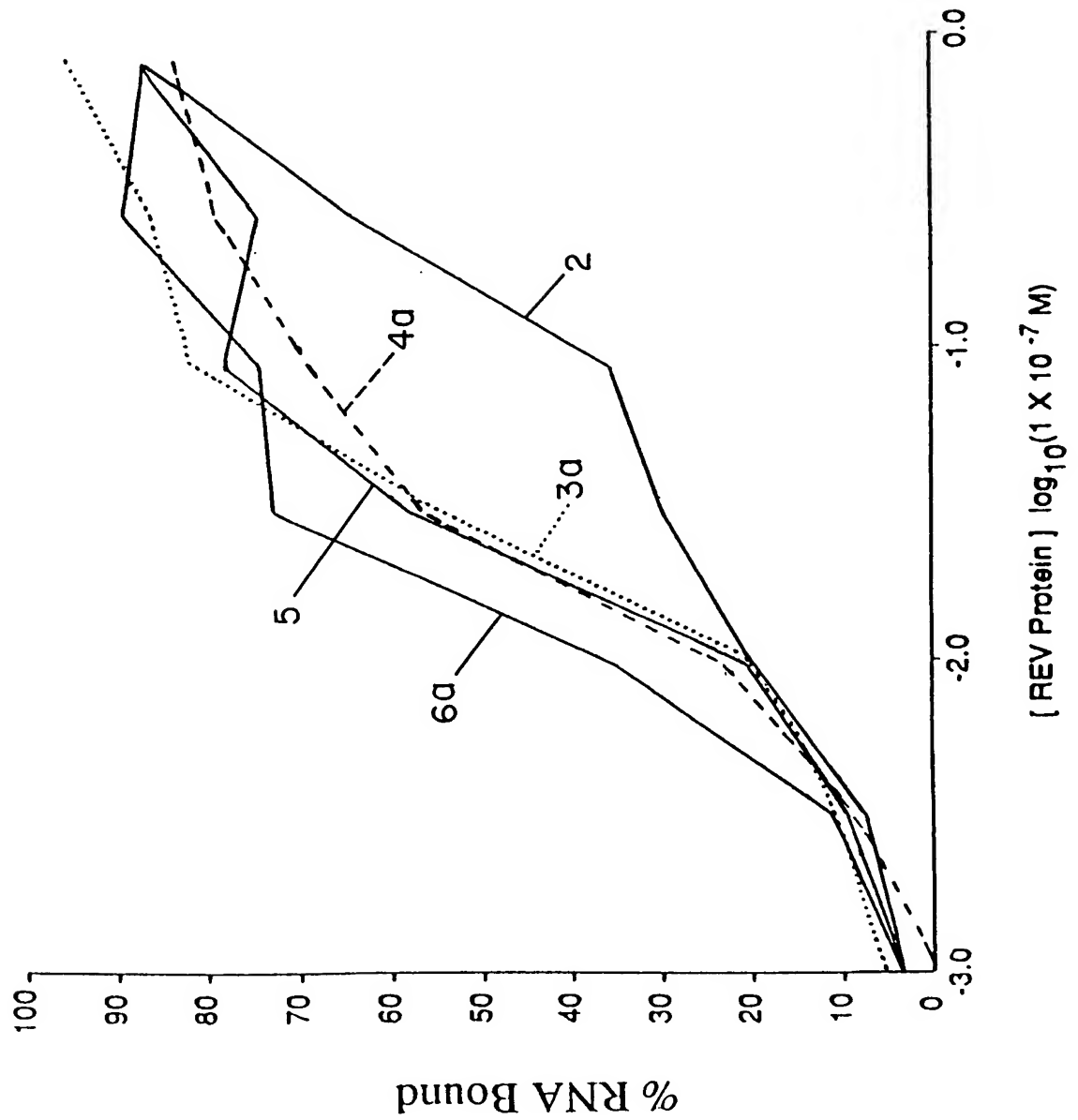
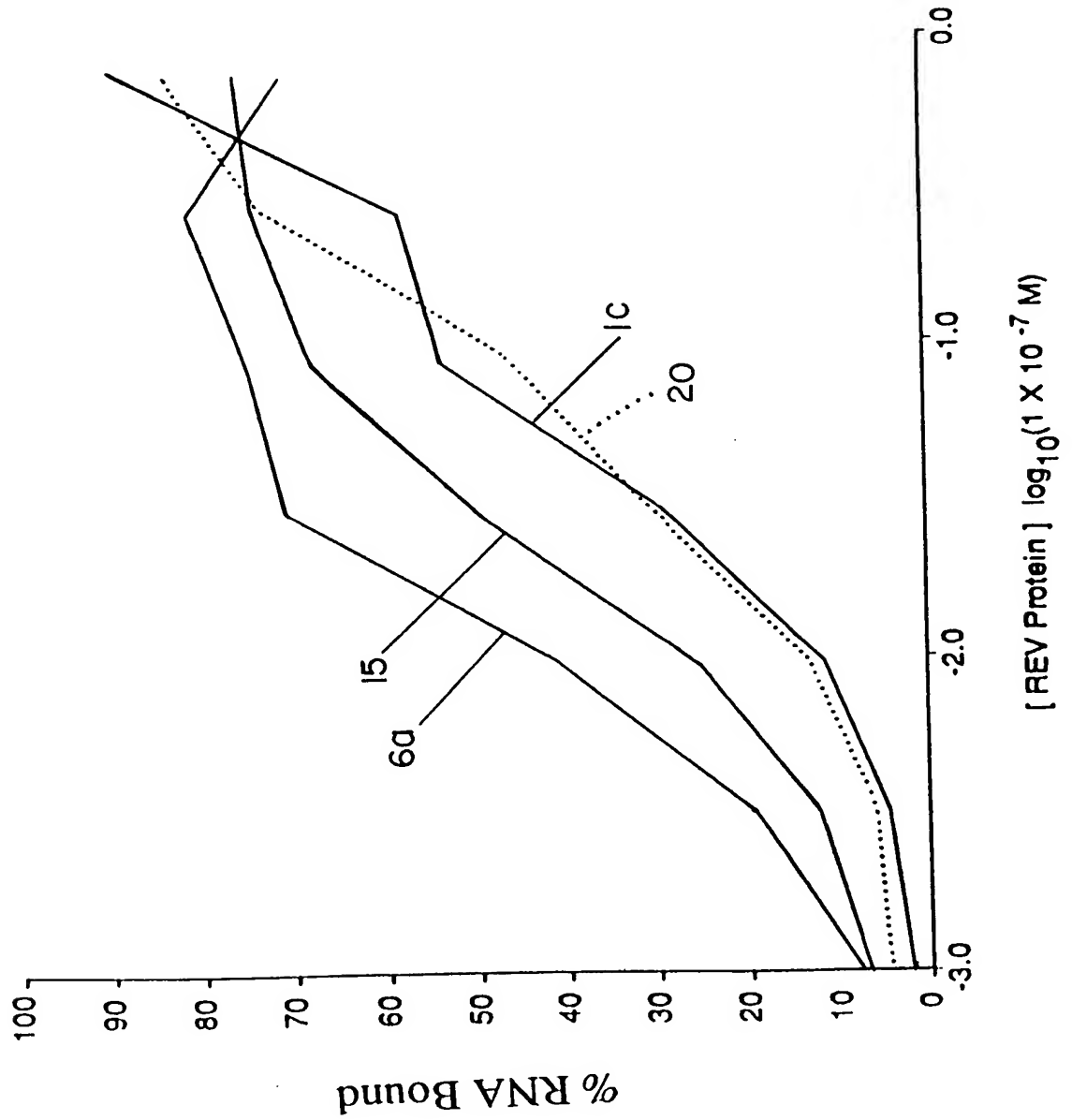


FIG.26



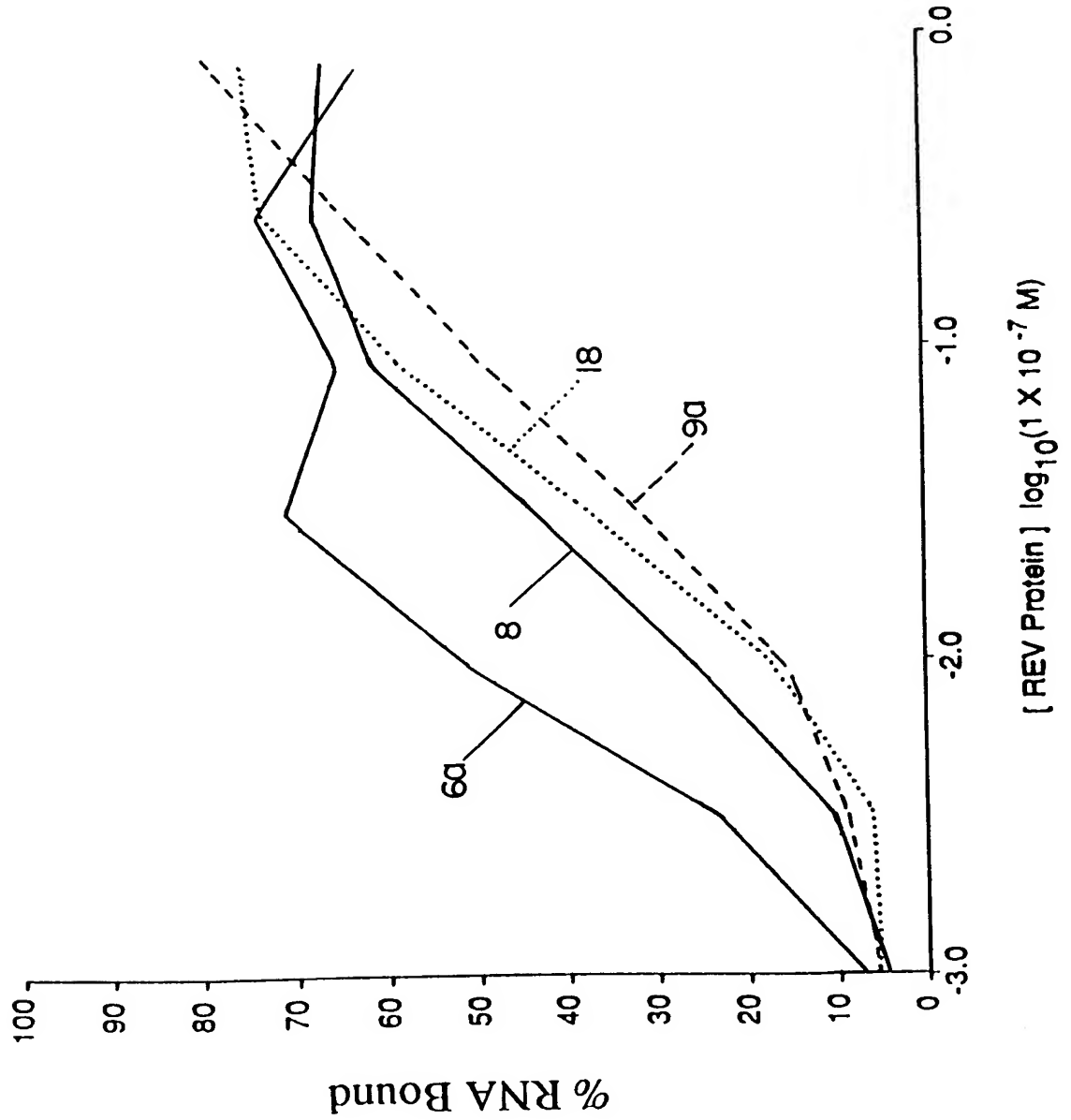
FOOT" 9864E00T

FIG.27



FOOT-9862E001

FIG. 28



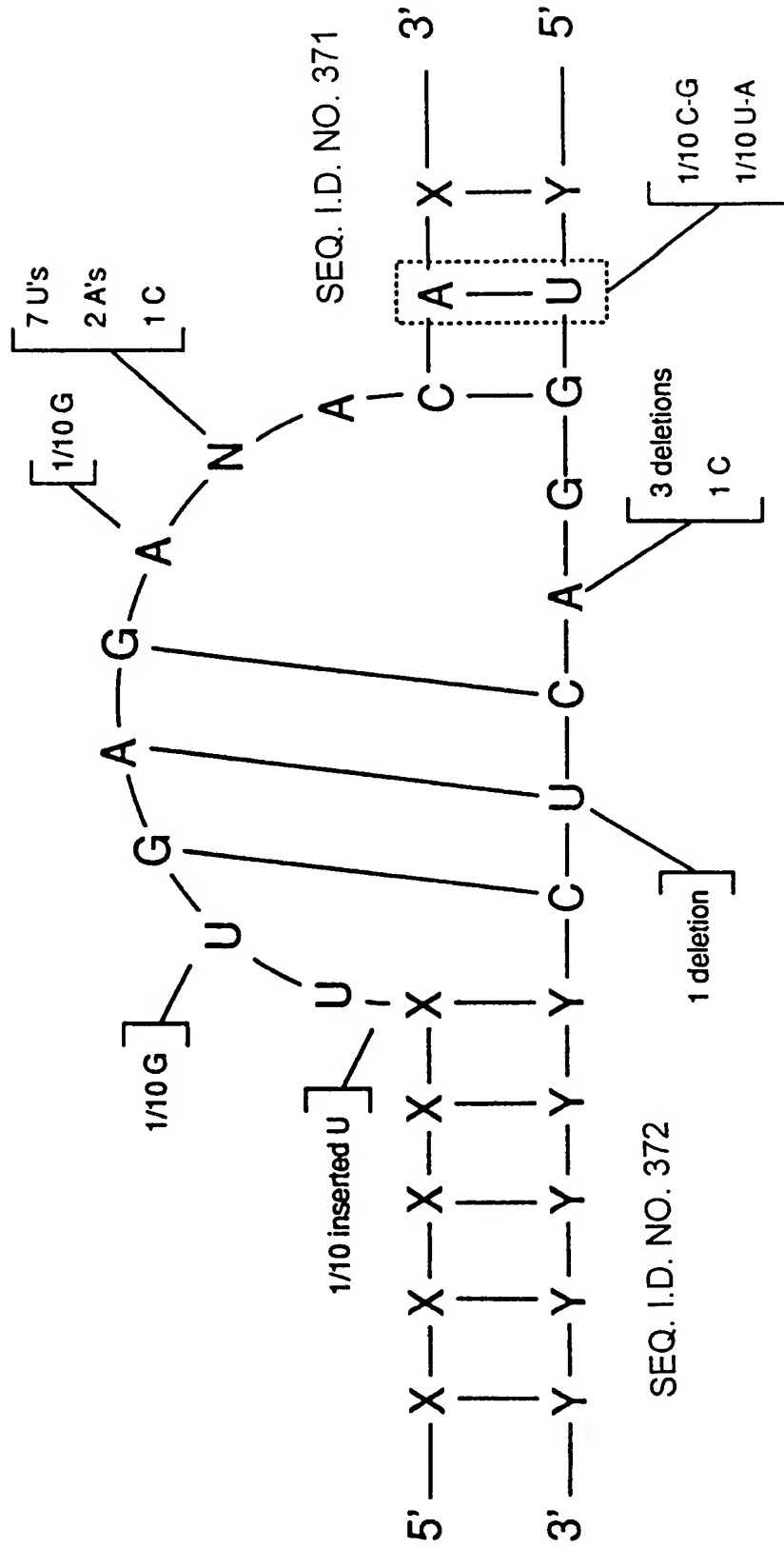
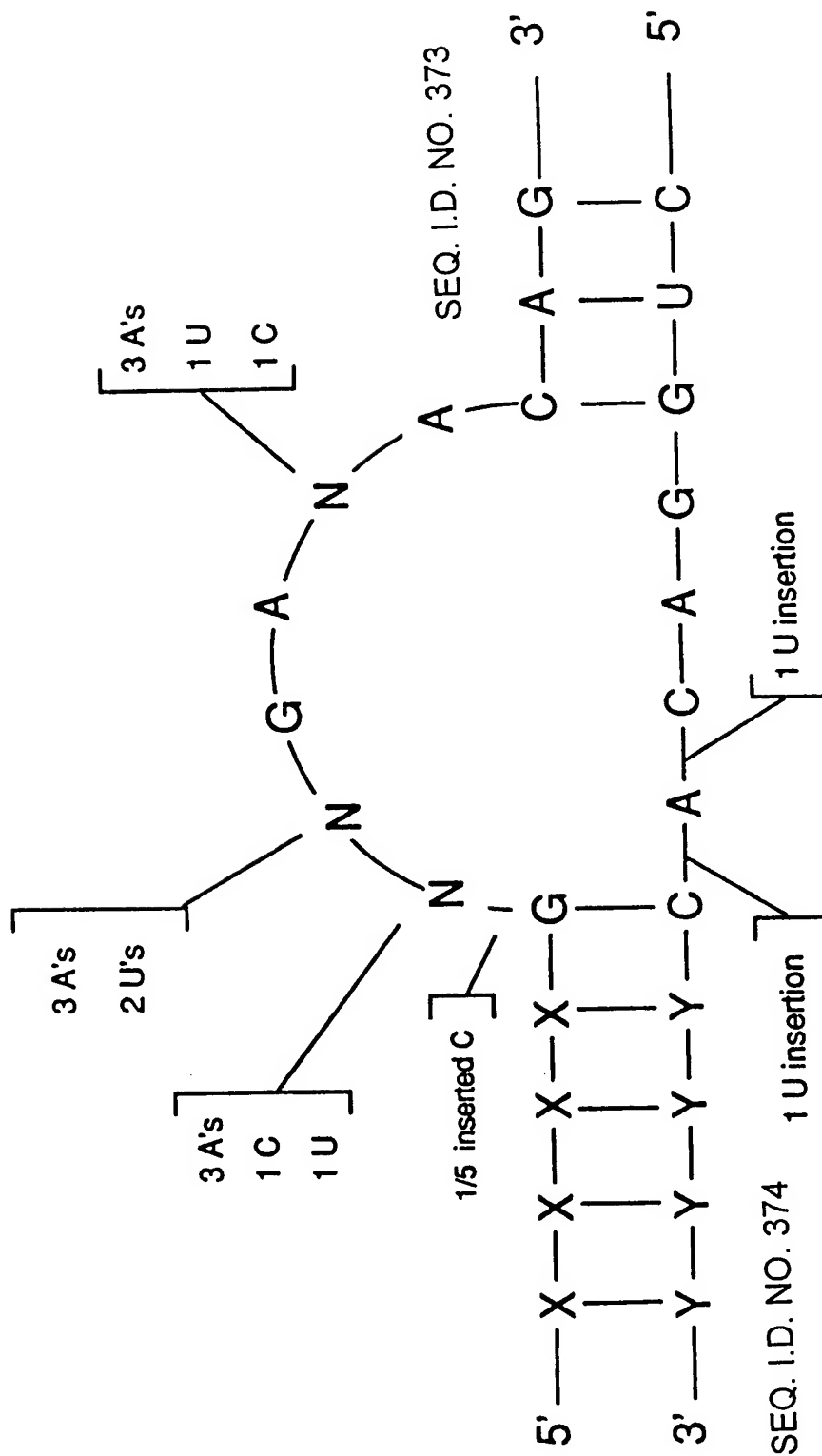


FIG. 29

FIG. 30



Motif II

